

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
 Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
 Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

**If more than one search is submitted, please prioritize searches in order of need.**

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

## STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>2</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>11/8/01</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>11/13/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>03</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

**This Page Blank (uspto)**

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2001, 16:23:06 ; Search time 2662.02 Seconds  
(without alignments)  
4342.942 Million cell updates/sec

Title: US-09-119-209-1  
Perfect score: 2259  
Sequence: 1 GAATTCAGAGTGTGTGCTT.....CCGCCAGCAGCTGGAATTC 2259

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues  
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
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80: gb\_vl2: \*  
81: gb\_pat1: \*  
82: gb\_pat2: \*  
83: em\_htg0: \*  
84: gb\_htg24: \*  
85: gb\_pr8: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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1	2259	100.0	2259	81 AR060685	AR060685 Sequence
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4	2127.8	94.2	2323	53 HSLFUR	X17519 Human mRNA
5	2087.6	92.4	2330	53 HSLYAM1	X16150 Human lymph
6	2087.6	92.4	2330	81 AR016679	AR016679 Sequence
7	2087.6	92.4	2330	81 AR040718	AR040718 Sequence
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13	1085.4	48.0	1119	85 PTU73729	U73729 Pongo pygma
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15	1037	45.9	1680	3 OCUC26535	U26535 Oryctolagus
16	970.2	42.9	141589	51 HSI17P20	AL021940 Homo sapi
17	963.8	42.7	2650	3 BTLECAM1	X62882 B.taurus mR
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## ALIGNMENTS

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RESULT 1
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LOCUS Sequence 1 from patent US 5840844.
DEFINITION AR060685
ACCESSION AR060685
VERSION AR060685.1 GI:5987135
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2259)
AUTHORS Laskey,L.A., Rosen,S.D., Stachel,S.E. and Slinger,M.S.
TITLE Soluble lymphocyte homing receptors
JOURNAL Patent: US 5840844-A 1 24-NOV-1998;
FEATURES
source location/Qualifiers
1..2259
BASE COUNT 635 a 517 c 488 g 619 t
ORIGIN
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Query Match Best Local Similarity 100.0%; Score 2259; DB 81; Length 2259; Matches 2259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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X16070  
ACCESSION X16070.1 GI:38092  
VERSION 1  
KEYWORDS lymphocyte adhesion receptor; lymphocyte homing receptor; transmembrane protein.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;

REFERENCE	1 (bases 1 to 2259)	Primates; Catarrhini; Homidae; Homo.
AUTHORS	Bowen, B.R., Nguyen, T., and Lasky, L.A.	
TITLE	Characterization of a human homologue of the murine peripheral lymph node homing receptor	
JOURNAL	J. Cell Biol. 109 (1), 421-427 (1989)	
MEDLINE	89308881	
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Db	2101	AAGAGTTAAACAGGTGGAGAAATTCCTTGATTACATGAAATGCTCTCTTTCCCTG	2160
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Db	2161	CCCCCGAAGCTTTPNCCACTTACCTAGATTCATATTCCTTAAATTTCAATCAGGC	2220
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RESULT 3

HOMLNHR

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

FEATURES

source

gene

sig\_peptide

2354 bp

mrna

07-OCT-1998

M25280

M25280.1

GI:187182

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 2354)

Siegelman, M.H. and Weissman, I.L.

Human homologue of mouse lymph node homing receptor: evolutionary conservation at tandem cell interaction domains

Proc. Natl. Acad. Sci. U.S.A. 86 (14), 5562-5566 (1989)

69315837

Draft entry and computer-readable sequence for [1] kindly provided by M.H.Sieglman, 02-JUN-1989.

location/Qualifiers

1..2354

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BASE COUNT 663 a 531 c 498 g 662 t

ORIGIN

Query Match 95.7%; Score 2161; DB 85; Length 2354;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 2200; Conservative 0; Mismatches 10; Indels 3; Gaps 3;

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QY 85 GCTCAATGGCGCTGCAGAGAACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 144  
DB 72 GCTCAATGGCGCTGCAGAGAACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 131

QY 145 AATGTCAGAGCAGCAG 204  
DB 132 AATGTCAGAGCAGCAG 191

QY 205 TCTGTGTGATTTCTGCGACATCATGGAACCTGCTGAGCTTACCATTAATTCGAAA 264  
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QY 325 CCATACAAAG 384  
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QY 1823 GACCATCTTATTTAAGTGGCTTCAAGGCTTCCCAACCTTCTTCAAGCAACCTCTCTTTTCA 1882

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QY	1943	ATAGCGCGGGGTTTTTTAGTTGGGGGTTTTGCTGTTTCTTTATGAGACCATTC	2002		APDLGIMNCSHPLASFSPSTACTFICSEGTLLGKRTTICSEGLSNFSPIQKLDK
Db	1931	ATAGCGCGGGGTTTTTTAGTTGGGGGTTTTGCTGTTTCTTTATGAGACCATTC	1990		SFEMIKRGDYNPLFIPIVAVWVTAFSGLAFIITLARRIKRKRSMNDPY
QY	2003	TATTTCTTATAGTCATGTTCTTTTATCAGCATATATATAGTAAGAACAATCAGTGA	2062		join(203, .1078,1515, .1574)
Db	1991	TATTTCTTATAGTCATGTTCTTTTATCAGCATATATATAGTAAGAACAATCAGTGA	2050		/note="Leu-8 is the human homologue of the mouse Mel-14
QY	2063	ATGCTACTGCAAGTCACATCTCTTGATGTCATATGGAAGATTAAACAGSTGGAGAA	2122		/product="Leu-8 antigen short form"
Db	2051	ATGCTACTGCAAGTCACATCTCTTGATGTCATATGGAAGATTAAACAGSTGGAGAA	2110		203, .1204
QY	2123	ATTCTGATTTCACATGAAATGCTCTCCCTTCCCTGCCCCAGAACCTTTATCCACTT	2182		/note="Leu-8 is the human homologue of the mouse Mel-14
Db	2111	ATTCTGATTTCACATGAAATGCTCTCCCTTCCCTGCCCCAGAACCTTTATCCACTT	2170		receptor"
QY	2183	ACCTAGATTCTACATATCTTTAAATTTGATCTCAGGCTCCCTCAACCCAC	2235		/product="Leu-8 antigen"
Db	2171	ACCTAGATTCTACATATCTTTAAATTTGATCTCAGGCTCCCTCAACCCAC	2223		BASE COUNT 652 a 520 c 490 g 661 t
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DEFINITION	Human mRNA for Leu-8 pan leukocyte antigen.				
ACCESSION	X17519				
VERSION	X17519.1	GI:34344			
KEYWORDS	antigen; glycoprotein; receptor; transmembrane protein.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
AUTHORS	Camerini, D., James, S.P., Stamenkovic, I. and Seed, B.				
TITLE	Leu-8/TOI is the human equivalent of the Mel-14 lymph node homing receptor				
JOURNAL	Nature 342 (6245), 78-82 (1989)				
MEDLINE	90044046				
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QY	104	AACATGAGAGAGGACCAAGCAACCATGATTTTCCATGGAATGTGAGAGCACCAGAG	163		APDLGIMNCSHPLASFSPSTACTFICSEGTLLGKRTTICSEGLSNFSPIQKLDK
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QY	224	ACATCATGAGACCTACTGCTGCACTTACATTTCTGAAAAACCATGAGACTGCAAG	283		/product="Leu-8 antigen short form"
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QY	464	GAACTGGGGAGATGTGAGCCCAACACAGAAAGAAAGAGAGAGCGGTGGAGATCTA	523		Best Local Similarity 99.38; Pred. No. 0;
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QY	704	GCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	763		
Db	664	GCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	723		
QY	764	CCCTTTGGAAGCTTCACTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	823		
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 DEFINITION Human Lym-1 mRNA for leukocyte adhesion molecule-1.  
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 KEYWORDS cell surface protein; leukocyte adhesion protein; transmembrane protein.

SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 2330)  
 AUTHOR T. F. Tedder  
 TITLE Direct Submission  
 JOURNAL Submitted (09-NOV-1989) Tedder T. F.  
 REFERENCE 2 (bases 1 to 2330)  
 AUTHORS Tedder, T. F., Isaacs, C. M., Ernst, T. J., Demetriou, G. D., Adler, D. A. and Distche, C. M.  
 TITLE Isolation and chromosomal localization of cDNAs encoding a novel human lymphocyte cell surface molecule, LAM-1. Homology with the mouse lymphocyte homing receptor and other human adhesion proteins  
 JOURNAL J. Exp. Med. 170 (1), 123-133 (1989)  
 MEDLINE 89310350  
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VERSION  
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SOURCE  
ORGANISM  
REFERENCE 1 (bases 1 to 2330)  
AUTHORS Tredder,T.F. and Sperdin,J.O.G.  
TITLE Anti-LAM 1-3 antibody and hybridoma  
JOURNAL Patent: US 5776775-A 1 07-JUL-1998;  
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Source 1..2330  
BASE COUNT 661 a 522 c 487 g 660 t  
ORIGIN

Query Match 92.4%; Score 2087.6; DB 81; Length 2330;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;

Oy 44 CCCTTTGGCAGACCTGAGACCTTGTGCTAGTCAAGAGGCTCAATGGGCTGCAGAG 103  
Db 7 CCTTTGGCAGAGACCTGAGACCTTGTGCTAGTCAAGAGGCTCAATGGGCTGCAGAG 66  
Oy 104 AACTAGAGAGGAGCAAGCAAGCCATGATATTTCATGGAATGTCAGAGCACCAGAG 163  
Db 67 AACTAGAGAGGAGCAAGCAAGCCATGATATTTCATGGAATGTCAGAGCACCAGAG 126  
Oy 164 GCACTTATGAGACATCTTCAAGTTGTGGGGTGAGCAATGCTGTGTGATTCCTGGC 223  
Db 127 GCACTTATGAGACATCTTCAAGTTGTGGGGTGAGCAATGCTGTGTGATTCCTGGC 186  
Oy 224 ACATCATGAGAACCTAGCTGAGACTTACATTTATCTGAAAAACCATGAACTGGCAAG 283  
Db 187 ACATCATGAGAACCGACTGAGACTTACATTTATCTGAAAAACCATGAACTGGCAAG 246  
Oy 284 GGCATAGAGATTCGCCGAGACAAATTCACAGATTTAGTTGCCATACAAAAAAGGGGGA 343  
Db 247 GGCATAGAGATTCGCCGAGACAAATTCACAGATTTAGTTGCCATACAAAAAAGGGGGA 306  
Oy 344 AATGAGATCTGAGAGAGACTGACCTTCAGTCTTACTACTAGTAGAATCCG 403  
Db 307 AATGAGATCTGAGAGAGACTGACCTTCAGTCTTACTACTAGTAGAATCCG 366  
Oy 404 GAGAGATGAGAGATATGAGAGTGGGTGGAGAACCAACAAATCTCTCACTGAAGAGAGA 463  
Db 367 GAGAGATGAGAGATATGAGAGTGGGTGGAGAACCAACAAATCTCTCACTGAAGAGAGA 426  
Oy 464 GAACCTGGGAGATGTCAGGCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 523  
Db 427 GAACCTGGGAGATGTCAGGCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 486

Oy 524 TATCAGAGAAAACAAGATGAGGCAAAATGAGAGTACGCTGCGACAACTAAAGGC 583  
Db 487 TATCAGAGAAAACAAGATGAGGCAAAATGAGAGTACGCTGCGACAACTAAAGGC 546  
Oy 584 AGCCCTCTGTACACAGCTTCTTGCCAGCCCTGGTCATGACAGTGGCCATGAGAAATGTGT 643  
Db 547 AGCCCTCTGTACACAGCTTCTTGCCAGCCCTGGTCATGACAGTGGCCATGAGAAATGTGT 606  
Oy 644 AGAATCATCAATATATCAGACCTGCACTGATGTGGGGGACTATGGGCCCCAGTGCA 703  
Db 607 AGAATCATCAATATATATACACCTGCACTGATGTGGGGGACTATGGGCCCCAGTGCA 666  
Oy 704 GCTTGTGATTCAGTGTAGAGCTTTGAGAGCCCGAGAGTGGGTACATGACACTGACTCA 763  
Db 667 GTTGTGTGATTCAGTGTAGAGCTTTGAGAGCCCGAGAGTGGGTACATGACACTGACTCA 726  
Oy 764 CCCCTTTGGAACCTTCACGCTTACAGCTGACGCTTCAGCTGCTGTGAGAGACAAA 823  
Db 727 CCCCTTTGGAACCTTCACGCTTACAGCTGACGCTTCAGCTGCTGTGAGAGACAAA 786  
Oy 824 CTTTAACTGGGATGAGAGAACACCTGTGAGCAATTTGGAACGTCATCTCCAGAAC 883  
Db 787 CTTTAACTGGGATGAGAGAACACCTGTGAGCAATTTGGAACGTCATCTCCAGAAC 846  
Oy 884 AACCTGTCAAGTATGATGAGTGTAGAGCTCTATCAGACACAGATTTGGGATCATGAATG 943  
Db 847 AACCTGTCAAGTATGATGAGTGTAGAGCTCTATCAGACACAGATTTGGGATCATGAATG 906  
Oy 944 TAGCCATCCCTGGCCAGCTTCACGCTTACCTGTGATGATGATGATGATGATGATGATG 1003  
Db 907 TAGCCATCCCTGGCCAGCTTCACGCTTACCTGTGATGATGATGATGATGATGATGATG 966  
Oy 1004 AACGAGTTAATGGAAGAAAGAAACCAATTTGGAATCATCTGGAATCTGCTGCAATTC 1063  
Db 967 AACGAGTTAATGGAAGAAAGAAACCAATTTGGAATCATCTGGAATCTGCTGCAATTC 1026  
Oy 1064 TAGTCAATATGTCAAAAAATTTGACAAAAGTTTCTCATGATTTAAGAGGGTGTATTA 1123  
Db 1027 TAGTCAATATGTCAAAAAATTTGACAAAAGTTTCTCATGATTTAAGAGGGTGTATTA 1086  
Oy 1124 CCCCTCTTCAATTCAGTGGCAGTCATGTTACTGCAATTCCTGCGTTGCGATTTATCAT 1183  
Db 1087 CCCCTCTTCAATTCAGTGGCAGTCATGTTACTGCAATTCCTGCGTTGCGATTTATCAT 1146  
Oy 1184 TTGGCTGGCAAGGATTTAAAAAAGCAAGAAATTCACAGAGATTTGCAATGACCCATA 1243  
Db 1147 TTGGCTGGCAAGGATTTAAAAAAGCAAGAAATTCACAGAGATTTGCAATGACCCATA 1206  
Oy 1244 TTAATGCCCCCTTGGTGAAGAAATTTCTGGAATTAATAAATCATGAGATCCCTTTAA 1303  
Db 1207 TTAATGCCCCCTTGGTGAAGAAATTTCTGGAATTAATAAATCATGAGATCCCTTTAA 1266  
Oy 1304 TCCTTCATGAACGTTTGT 1362  
Db 1267 TCCTTCATGAACGTTTGT 1326  
Oy 1363 TTCAGTGCATCTGGAGAGATTTTACCCGACCAACAGTTCCTTACGTTCCATTTCCGCC 1422  
Db 1327 TTCAGTGCATCTGGAGAGATTTTACCCGACCAACAGTTCCTTACGTTCCATTTCCGCC 1386  
Oy 1423 CTCATTTATCCCTCAACCCCGACGCTGTTTATACAGTCACTTTTGTCTTTT 1482  
Db 1387 CTCATTTATCCCTCAACCCCGACGCTGTTTATACAGTCACTTTTGTCTTTT 1446  
Oy 1483 CTGAGAGAAAACAATTAAGACAT -AAGGAAAGAGATTCATGTGGAATTAAGATGGCT 1541  
Db 1447 CTGAGAGAAAACAATTAAGACATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1506  
Oy 1542 GACTTGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1601  
Db 1507 GACTTGTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1566  
Oy 1602 ACATCTTAATGAAAGTCAAAATTTGATACATATGTAATATGAGACTGACTTTCTTGA 1661



QY	104	AACTGAGAAAGACCAAGCAAAAGCAGATATTTCCATGGAATGTCAAGACCCACAG	16
Db	67	AACTAGAAAGAGCCAAAGCAAGCCAGATATTTCCATGGAATGTCAAGACCCACAG	126
QY	164	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGGACAATGCTGTGTGATTTCTGGC	22
Db	127	GGACTTATGGAACATCTTCAAGTTGTGGGGGTGGACAATGCTGTGTGATTTCTGGC	186
QY	224	ACATCATGGAACCTACTGCTTGACCTTACCATTTATCTGAAAAAACCATGAATGGCAAG	283
Db	187	ACATCATGGAACCGACAGCTGCGACTTACCATTTATCTGAAAAAACCATGAATGGCAAG	246
QY	284	GGCTAGAGAAGATTTGCGCGAATACATTTACACATTTAGTGTGCATACAAAACAGCGGA	343
Db	247	GGCTAGAGAAGATTTGCGCGAATACATTTAGTGTGCATACAAAACAGCGGA	306
QY	344	AATTGAGTATCTGAGAAAGACTGTGCCCTTCAGTGGTTCTTACTACTGATAGGAATCCG	403
Db	307	AATTGAGTATCTGAGAAAGACTGTGCCCTTTCAGTGGTTCTTACTACTGATAGGAATCCG	366
QY	404	GAAGATGTGAGGAATATGAGCGTGGGTGGGAACCAAAATCTCTCACTAAGAAAGCA	463
Db	367	GAAGATGTGAGGAATATGAGCGTGGGTGGGAACCAAAATCTCTCACTAAGAAAGCA	426
QY	464	GAATGGGGGAGTGTGAGCCCAACAAAGAAAGAACAGAGGAGTGTGCTGAGATCTA	523
Db	427	GAATGGGGGAGTGTGAGCCCAACAAAGAAAGAACAGAGGAGTGTGCTGAGATCTA	486
QY	524	TATCAAGAGAAACAAAGATGCGAGCAATGTGAAGATGAGCGCTGCCACAATAAGGC	583
Db	487	TATCAAGAGAAACAAAGATGCGAGCAATGTGAAGATGAGCGCTGCCACAATAAGGC	546
QY	584	AGCCCTCTGTACACAGCTTCTTGGCACCCCTGTCTCATGCAAGTGGCCATGGAATGTGT	643
Db	547	AGCCCTCTGTACACAGCTTCTTGGCACCCCTGTCTCATGCAAGTGGCCATGGAATGTGT	606
QY	644	AGAAATCATCATATATATCACACCTGTGACACTGTGATGTGGGTACTATGGGCCCACTGCA	703
Db	607	AGAAATCATCATATATATATCACACCTGTGACACTGTGATGTGGGTACTATGGGCCCACTGCA	666
QY	704	GCTTGTGATTCAGTGTGAGCCTTTGGAGGCCCCAGACTGGTACCATGAGACTGTACCA	763
Db	667	GCTTGTGATTCAGTGTGAGCCTTTGGAGGCCCCAGACTGGTACCATGAGACTGTACCA	726
QY	764	CCCCCTTGGAACTTCAAGCTTCAAGCTCACAGTGTGCTTACAGTGTCTGAAGAACAACAA	823
Db	727	CCCCCTTGGAACTTCAAGCTTCAAGCTCACAGTGTGCTTACAGTGTCTGAAGAACAACAA	786
QY	824	CTTAACTGGGATTTGAAGAAACCACTGTGGACCATTTGGAAACTGTCTATCTCCAGAAC	883
Db	787	CTTAACTGGGATTTGAAGAAACCACTGTGGACCATTTGGAAACTGTCTATCTCCAGAAC	846
QY	884	AACTGTCAAGTATTCAGTGTGAGCCTTATCAGCACCAAGATTTGGGGATCATGAATGTG	943
Db	847	AACTGTCAAGTATTCAGTGTGAGCCTTATCAGCACCAAGATTTGGGGATCATGAATGTG	906
QY	944	TAGCATTCCCTGCGCAGCTTCAAGCTTTACCTTCGATGTACCTTCAATCTGTCAAGAG	1003
Db	907	TAGCATTCCCTGCGCAGCTTCAAGCTTTACCTTCGATGTACCTTCAATCTGTCAAGAG	966
QY	1004	AACTGAGTTAATTTGGGAAGAAACCAATTTGTGAATCATCTGGAATCTGTGCAAAATCC	1063
Db	967	AACTGAGTTAATTTGGGAAGAAACCAATTTGTGAATCATCTGGAATCTGTGCAAAATCC	1026
QY	1064	TAGTCCAAATATGCAAAAATTTGACAAAAGTTTCTCAATGATTTAAGAGGGGTATTATAA	1123
Db	1027	TAGTCCAAATATGCAAAAATTTGACAAAAGTTTCTCAATGATTTAAGAGGGGTATTATAA	1086
QY	1124	CCCCCTTATATTCACAGTGGCACTATGTTTCACGATTTCCCTGGGTGGCATTTATCAT	1183
Db	1087	CCCCCTTATATTCACAGTGGCACTATGTTTCACGATTTCTCTGGGTGGCATTTATCAT	1146



QY	1184	TTCTCTGGCAAGGAGATTAAAAAAAGGCAAGAAATTCACAGAGAACTATGATGACCCCTA	1243
Db	1147	TTGGCTGGCAAGGAGATTAAAAAAGGCAAGAAATTCACAGAGAACTATGATGACCCCTA	1206
QY	1244	TTAATAGCCCTTGGTGGAAGAAATTCCTGGAAATCTAAATATCATGATCCCTTAA	1303
Db	1207	TTAAATGCCCCCTTGGTGGAAGAAATTCCTGGAAATCTAAATATCATGATCCCTTAA	1266
QY	1304	TCCTTCATGAAGACGTTTGTGTGGGACCTCTACGTCMAACATGAGTGTG - TTCC	1362
Db	1267	TCCTTCATGAAGACGTTTGTGTGGGACCTCTACGTCMAACATGAGTGTGTCC	1326
QY	1363	TTTCAGTCGATCTGGGAAGATTTTACCAGCAACAGTTCTTTACGTTCCATTTCCGCC	1422
Db	1327	TTTCAGTCGATCTGGGAAGATTTTACCAGCAACAGTTCTTTACGTTCCATTTCCACC	1386
QY	1423	CTCATTTATCCCTCAACCCCAAGGCGGTTATACACTCAGCTTTTGTGCTTT	1482
Db	1387	CTCATTTATCCCTCAACCCCAAGGCGGTTATACACTCAGCTTTTGTGCTTTT	1446
QY	1483	CTGAGGAGAAACAATTAAGACAT - AAGGGAAAGATTATGATGAAATTAAGTGGCT	1541
Db	1447	CTGAGGAGAAACAATTAAGACATTAAGGAAAGATTATGATGAAATTAAGTGGCT	1506
QY	1542	GACTTTGCTCTTTCTTGACCTCTGTTTTCAGTTTCAATTCAGTGTGATGATGACAG	1601
Db	1507	GACTTTGCTCTTTCTTGACCTCTGTTTTCAGTTTCAATTCAGTGTGATGATGACAG	1566
QY	1602	ACACTCTAAATGAAGGCAAAATTATACATATGTAATATGAGCTCAGTTTCTTGCA	1661
Db	1567	ACACTCTAAATGAAGGCAAAATTTATATGTAATATGAGCTCAGTTTCTTGCA	1626
QY	1662	GATCAAAATTCAGCTGCTCTTCTGTACTGTGGAGGTACACTTAAGAAGTTCAA	1721
Db	1627	GATCAAAATTCGGGTGCTCTTCTGTATAC - GTGGAGGTACACTCT - - - - ATGAAGTCAA	1680
QY	1722	AAGTCACGCTCTCTCTTTCTTAACTCAGTGAAGTAAAGGGGCTCGTCAAGTTGA	1781
Db	1681	AAGTCACGCTCTCTCTTTCTTAACTCAGTGAAGTAAAGGGGCTCGTCAAGTTGA	1740
QY	1782	AAGAGTCCTATTGTGCACTGAGCTGGCGGTCTGTGAATATGAGCACTCTATTACGTG	1841
Db	1741	AAGAGTCCTATTGTGCACTGAGCTGGCGGTCTGTGAATATGAGCACTCTATTAACTGG	1800
QY	1842	CTTAGGCGTCCCAACCTCTTTAGGCACCTGCTTTCAATGGGTGACTCCACACC	1901
Db	1801	CTTAGGCGTCCCAACCTCTTTAGGCACCTCTCTTTTTCAGTGTGGCTGACTCCACACC	1859
QY	1902	TGACATCTCATGACTGGCAGCAAAAAGAGAGAGAGAAATAGCTCGCGGGTTTTTTT	1961
Db	1860	TGACATCTCATGAGTGGCAGCAAAAAGAGAGAGAGAAATAGCTCGCGGGTTTTTTT	1919
QY	1962	AGTTTGGGGGTTTTTGGCTTTTCTTTTATGAGACCCATTCCTATTCTTATATGTCATGT	2021
Db	1920	AGTTTGGGGGTTTTTGGCTTTTCTTTTATGAGACCCATTCCTATTATGTCATATGT	1979
QY	2022	TTCTTTATACAGATATTTATTAAGAAACAATCATACGTAATGTCTACTCAAGTAGCA	2081
Db	1980	TTCTTTATACAGATATTTATTAAGAAACAATCATCTGAATGTCTACTCAAGTAGCA	2039
QY	2082	TCCTTTGATGATCATATGAGAGATTAAACAGAGTGGAGAAATTCCTTGATTCACAATGA	2141
Db	2040	TCCTTTGATGATCATATGAGAGATTAAACAGAGTGGAGAAATTCCTTGATTCACAATGA	2099
QY	2142	AATGCTCTCTTTTCCCTGGCCCAAGAACTTTTATCCATTACCTAGATCTACATATTC	2201
Db	2100	AATGCTCTCTTTTCCCTGGCCCAAGAACTTTTATCCATTACCTAGATCTACATATTC	2159
QY	2202	TTTAAATTTGATCTCAGGCGCTCCCTCAACCCAC	2235
Db	2160	TTTAAATTTGATCTCAGGCGCTCCCTCAACCCAC	2193

[illegible]

QY	764	CCCCCTTGGAAACTGACGCTTCACTGACACAGTGTGCTTCAGCTGCTCTGTAAGGACAAA	823
Db	727	CCCTTTGGGAAACCTTCAACTCTCAACCTACACAGTGTGCTTCAGCTGCTCTGTAAGGACAAA	786
QY	824	CTTAACCTGGGATTGGAAGAACCCACCTGTGTGACCATTTGGAAACGTGTCACTCCAGAAC	883
Db	787	CTTAACCTGGGATTGGAAGAACCCACCTGTGTGACCATTTGGAAACGTGTCACTCCAGAAC	846
QY	884	AACCTGTCAAGTCAATTCAGTGTGAGCTCTCATCAGCACACAGATTTGGGGATCATGAACCTG	943
Db	847	AACCTGTCAAGTCAATTCAGTGTGAGCTCTCATCAGCACACAGATTTGGGGATCATGAACCTG	906
QY	944	TAGCATCCCCCTGGCCAGCTGTGACGCTTAAACCTGTGCATGTACCTCATCTGTCTCAAGAG	1007
Db	907	TAGCATCCCCCTGGCCAGCTGTGACGCTTAAACCTGTGCATGTACCTCATCTGTCTCAAGAG	966
QY	1004	AACCTAGTTAATTTGGGAGAAGAAACCAATTTGTGAATCATCTGTGATCTGGTGCATATCC	1067
Db	967	AACCTAGTTAATTTGGGAGAAGAAACCAATTTGTGAATCATCTGTGATCTGGTGCATATCC	1022
QY	1064	TAGTCCAAATTTGTGCAAAATTTGGAGAAAAGTTTCTCAATGATTTAGAGGGGTGATTAATA	1122
Db	1027	TAGTCCAAATTTGTGCAAAATTTGGAGAAAAGTTTCTCAATGATTTAGAGGGGTGATTAATA	1086
QY	1124	CCCCCTCTTCATCTCAGTGTGACGATGATGTTACGACATCTCTGCTGGGTGGCATTTATCT	1187
Db	1087	CCCCCTCTTCATCTCAGTGTGACGATGATGTTACGACATCTCTGCTGGGTGGCATTTATCT	1146
QY	1184	TTGGCTGGGACAGAGATTTAAAAAAGGCAGAAATCCAGAGAGATTAATGATACCCTATA	1243
Db	1147	TTGGCTGGGACAGAGATTTAAAAAAGGCAGAAATCCAGAGAGATTAATGATACCCTATA	1206
QY	1244	TTTAAATCGCCTTGGTGAAGAAAATTTCTTGGAATACTAAATTCATGATGATCCCTTTAA	1303
Db	1207	TTTAAATCGCCTTGGTGAAGAAAATTTCTTGGAATACTAAATTCATGATGATCCCTTTAA	1266
QY	1304	TCCTTCGATGAAACGTTTGTGTGTGTGACACTCTCTACGTCAAACATGAAAGTGTG-TTCC	1362
Db	1267	TCCTTCGATGAAACGTTTGTGTGTGTGACACTCTCTACGTCAAACATGAAAGTGTGTTC	1326
QY	1363	TTTCAGTGCATCTGGGAGAAATTTTACCCGACCAAGAGTTCTTCAGCTTCCATTTTCCGCC	1422
Db	1327	TTTCAGTGCATCTGGGAGAAATTTTACCTGTGACCAAGTTCTTCAGCTTCCATTTTCCGCC	1386
QY	1423	CTCATTTTATCCCTCAACCCCGACCCACAGAGTGTATACAGCTCAGCTTTTGTGCTTTT	1482
Db	1387	CTCATTTTATCCCTCAACCCCGACCCACAGAGTGTATACAGCTCAGCTTTTGTGCTTTT	1446
QY	1483	CTGAGAGAAACAAATTAAGACCAT-TAAGGAAAGATTCATGTGGAATATAAGATGGCT	1541
Db	1447	CTGAGAGAAACAAATTAAGACCATTAAGGAAAGATTCATGTGGAATATAAGATGGCT	1506
QY	1542	GACTTGTCTTTCTTGACACTTGTATTAGTTCAATTCATCTGATCTGATCTGATGACAG	1601
Db	1507	GACTTGTCTTTCTTGACACTTGTATTAGTTCAATTCATCTGATCTGATCTGATGACAG	1566
QY	1602	ACACTTCAATTAAGAGCAAAATTTATACATATGTGAATATGACATCAGTTTCTTGCA	1661
Db	1567	ACACTTCAATTAAGAGCAAAATTTATACATATGTGAATATGACATCAGTTTCTTGCA	1626
QY	1662	GATCAAAATTTACACTGCTCTCTGTATACGTGTGAGAGTCACTCTTATAGAACTTCAA	1721
Db	1627	GATCAAAATTTGCGGTGCTCTGTGTATAC-GTGGAGTTCACCTCT-----ATGAAGTCAA	1680
QY	1722	AAGTCTACGCTCTCTTTCTTTCTAATCTCAGTGAAGTAATGGGGTCTGTCTCAAGTTGA	1781
Db	1681	AAGTCTACGCTCTCTTTCTTTCTAATCTCAGTGAAGTAATGGGGTCTGTCTCAAGTTGA	1740
QY	1782	AAGAGTCTTATTTGGCACTGAGAGCTGCGCGCTGTGGAATTTGGACATCTCTAATTAACGTG	1841
Db	1741	AAGAGTCTTATTTGGCACTGAGAGCTGCGCGCTGTGGAATTTGGACATCTCTAATTAACGTG	1800

QY	1842	CTTGCAGGCGCTCCCGACCTTCTCTTCAGCGCACCTCTCTTTTTCAGTTGGGCTGCATTTCCACAC	1901
Db	1801	CTTCA-GCGCTCCCGACCTTCTCTTCAGCGCACCTCTCTTTTTCAGTTGGGCTGCATTTCCACAC	1859
QY	1902	TAGCATCTCATATAGTGGCCAGCAAAAGGAGAGACAGAAATACCTGGCGGGTTTTTT	1961
Db	1860	TAGCATCTCATATAGTGGCCAGCAAAAGGAGAGAGAAATACCTGGCGGTGTTTTT	1919
QY	1962	AGTTTGGGGGTTTTGCTGTTTTCTTTTATGAGACCCATTTCCATTTATATAGTCAATGT	2021
Db	1920	AGTTTGGGGGTTTTGCTGTTTTCTTTTATGAGACCCATTTCCATTTATATAGTCAATGT	1979
QY	2022	TTCTTTATACAGATATATTAGTAGAAACATACAGAAATGTACTGCAAGTACA	2081
Db	1980	TTCTTTATACAGATATATTAGTAGAAACATACAGAAATGTACTGCAAGTACA	2039
QY	2082	TCTCTTATATGTCATATATGGAAGAGTTAAACAGGTGAGAAATTCCTTGATTCACAAATGA	2141
Db	2040	TCTCTTATATGTCATATATGGAAGAGTTAAACAGGTGAGAAATTCCTTGATTCACAAATGA	2099
QY	2142	AATGCTCTCTTCCCGCCGCCAGACCTTTTATCCACTTACTAGATTCTACATATTC	2201
Db	2100	AATGCTCTCTTCCCGCCGCCAGACCTTTTATCCACTTACTAGATTCTACATATTC	2159
QY	2202	TTTAATTTTCATCTCAGGCGCTCCCTCAACCCAC	2235
Db	2160	TTTAATTTTCATCTCAGGCGCTCCCTCAACCCAC	2193
RESULT	9		
I70140	I70140	2330 bp	DNA
LOCUS	Sequence	1	from patent US 5679346.
DEFINITION	I70140		
ACCESSION	I70140.1	GI:3006275	
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			Unknown.
REFERENCE			Unclassified.
AUTHORS			1 (bases 1 to 2330)
TITLE			Tedder,T.F. and Spertini,O.G.
JOURNAL			Methods of blocking adhesion with anti-lami-3 antibody
FEATURES			Patent: US 5679346-A.1 21-OCT-1997;
			Location/Qualifiers
			1..2330
			/organism="unknown"
BASE COUNT	661 a	522 c	487 g
ORIGIN			660 t
Query Match	92.4%;	Score 2087.6;	DB 81; length 2330;
Best Local Similarity	98.5%;	Pred. No. 0;	
Matches 2161; Conservative	0;	Mismatches 24;	Indels 9; Gaps
QY	44	CCCTTTGGCAAGGACCTGTGAGACCTTGTCTTAAGTCAAGAGGCTCAATGGGCTGCAGAG	103
Db	7	CCTTTGGCAAGGACCTGTGAGACCTTGTCTTAAGTCAAGAGGCTCAATGGGCTGCAGAG	66
QY	104	AACATAGAGAAGGACCAAGCAAAAGCCATGATATTTCCATGAGAAATGTCAAGAGCACCAAG	163
Db	67	AACATAGAGAAGGACCAAGCAAAAGCCATGATATTTCCATGAGAAATGTCAAGAGCACCAAG	126
QY	164	GGACTTATGGAACATCTTCAAGTGTGGGGGGTGGACAAATGCTGTGTGTGATTTCTTGGC	223
Db	127	GGACTTATGGAACATCTTCAAGTGTGGGGGGTGGACAAATGCTGTGTGTGATTTCTTGGC	186
QY	224	ACATCATGGAACCTTACTGCTGACTTACCATTTATTTCTGAAAAACCATGAACTGGCAAG	283
Db	187	ACATCATGGAACCGACTGCTGACTTACCATTTATTTCTGAAAAACCATGAACTGGCAAG	246
QY	284	GGCTTGAAGATTCTGGCGGAGCAATTTACACAGATTTTACTTGCATACAAAACAGCGCGA	343
Db	247	GGCTTGAAGATTCTGGCGGAGCAATTTACACAGATTTTACTTGCATACAAAACAGCGCGA	306

QY	344	AATTGAGTATCTTGAGAGAAAGCTCTGCCCTTCAGTCTTCTTACTACTGGATAGGAATCCG	403
Db	307	AATTGGATCTTGAGAGAAAGCTCTGCCCTTCAGTCTTCTTACTACTGGATAGGAATCCG	366
QY	404	GAAAGATAGAGAGAAATTTGGACGTGGGTGGGAAACCAACAAATCTCTCACTGAAGACAGA	463
Db	367	GAAAGATAGAGAGAAATTTGGACGTGGGTGGGAAACCAACAAATCTCTCACTGAAGACAGA	426
QY	464	GAACCTGGGAGATGCTGAGACCCCAACAAGAAAGACAGAGAGAGCTGCTGGAGATCTTA	523
Db	427	GAACCTGGGAGATGCTGAGACCCCAACAAGAAAGACAGAGAGAGCTGCTGGAGATCTTA	486
QY	524	TATTCAGAGAAACAAAGATGACAGCAAAATGGAATGACGCTGCCAACAACCTTAAGGC	583
Db	487	TATTCAGAGAAACAAAGATGACAGCAAAATGGAATGACGCTGCCAACAACCTTAAGGC	546
QY	584	AGCCCTCTTTACAGAGCTTTTGGCAGGCCCTGGTATGATGAGTGGCATTGGAATATGT	643
Db	547	AGCCCTCTTTACAGAGCTTTTGGCAGGCCCTGGTATGATGAGTGGCATTGGAATATGT	606
QY	644	AGAAATCATCAATTAATCACACACCTGCAACTGTGATGGGGTACTATGGGCCCAAGTCTCA	703
Db	607	AGAAATCATCAATTAATTAACACCTGCAACTGTGATGGGGTACTATGGGCCCAAGTCTCA	666
QY	704	GCTTGTGATTCAGTGTGAGCCTTTGGAGGCCCAAGAGCTGGATGACATGAGCTGTACTCA	763
Db	667	GTTTGTGATTCAGTGTGAGCCTTTGGAGGCCCAAGAGCTGGATGACATGAGCTGTACTCA	726
QY	764	CCCCCTTGGAAACTTACGCTTCACGTCACAGTGTGCTTACGCTGTCTGAAGAAACAA	823
Db	727	CCCCCTTGGAAACTTACGCTTCACGTCACAGTGTGCTTACGCTGTCTGAAGAAACAA	786
QY	824	CTTAACTGGGATTTGAAGAAACACACCTGTGAGACATTTGGAACTGGCATCTGCAGAAC	883
Db	787	CTTAACTGGGATTTGAAGAAACACACCTGTGAGACATTTGGAACTGGCATCTGCAGAAC	846
QY	884	AACTGTCAAGTATTCAGTGTGAGCCTCTATCAGCAGCAGATTTGGGATTCATGAACTG	943
Db	847	AACTGTCAAGTATTCAGTGTGAGCCTCTATCAGCAGCAGATTTGGGATTCATGAACTG	906
QY	944	TAGCCATCCCTGGCCAGCTTTCAGCTTACCTGTGCATGACCTTATCTGTCTCAGAGG	1003
Db	907	TAGCCATCCCTGGCCAGCTTTCAGCTTACCTGTGCATGACCTTATCTGTCTCAGAGG	966
QY	1004	AACTGAGTTAATTTGGGAAAGAAACCAATTTGTAATCATCTGGAATCGTCAATATCC	1063
Db	967	AACTGAGTTAATTTGGGAAAGAAACCAATTTGTAATCATCTGGAATCGTCAATATCC	1026
QY	1064	TAGTCCAAATATGTCAAAAATTTGGACAAAGTTTCTCAATGATTAAAGAGGGTATTATA	1123
Db	1027	TAGTCCAAATATGTCAAAAATTTGGACAAAGTTTCTCAATGATTAAAGAGGGTATTATA	1086
QY	1124	CCCCCTTTCATTTCCAGTGGCAGTCAATGTTACTGCAATTCCTGGGTTGGCATTTATCAT	1183
Db	1087	CCCCCTTTCATTTCCAGTGGCAGTCAATGTTACTGCAATTCCTGGGTTGGCATTTATCAT	1146
QY	1184	TTGGGCTGGCAAGAGATTTAAAAAAGCAAGAAATTCACAGAGAGATGAATGACCCATA	1243
Db	1147	TTGGGCTGGCAAGAGATTTAAAAAAGCAAGAAATTCACAGAGAGATGAATGACCCATA	1206
QY	1244	TTTAAATCGCCCTTGGTGAAGAAATTTCTTGGAAATCTATAAATCATGAGATCTTTTAA	1303
Db	1207	TTTAAATCGCCCTTGGTGAAGAAATTTCTTGGAAATCTATAAATCATGAGATCTTTTAA	1266
QY	1304	TTCTTCATGAAGAGTTTGTGTGTGTCACCTCTACGTCAAAATGAAGTGTG-TTCC	1362
Db	1267	TTCTTCATGAAGAGTTTGTGTGTGTCACCTCTCTACGTCAAAATGAAGTGTGTGTTCC	1326
QY	1363	TTTCAGTGCATCTGGGAAAGTTTCTACCCGACCAACAGTTCTTTCACACTTCCATTTTGGCC	1422
Db	1327	TTTCAGTGCATCTGGGAAAGTTTCTACCTCAACACAGTTCTTTCACACTTCCATTTTACC	1386

TITLE Direct Submission  
JOURNAL Submitted (04-SEP-1999) Fieger C.B., Benjamin Franklin Klinikum der  
Freien Universitaet Berlin, Institut fuer Klinische Chemie &  
Pathobiochemie, Hindenburgdamm 30, 12200 Berlin, GERMANY

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BASE COUNT 463 a 338 c 364 g 404 t

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Query Match 67.8%; Score 1532.2; DB 52; Length 1569;  
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Matches 1559; Conservative 0; Mismatches 8; Indels 2; Gaps 2;

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Db	1561	ATGAAGTGC	1569
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LOCUS	PHU52074	1510 bp	mRNA
DEFINITION	Papio hamadryas anubis L-selectin precursor mRNA, complete cds.		
ACCESSION	U52074		
VERSION	U52074.1	GI:1326148	
KEYWORDS			
SOURCE	olive baboon.		
ORGANISM	Papio hamadryas anubis		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
	Cercopithecinae; Papio.		
REFERENCE	1 (bases 1 to 1510)		
AUTHORS	Tsurushita, N., Fu, H. and Berg, E.L.		
TITLE	PCR cloning of the cDNA encoding baboon L-selectin		
JOURNAL	Gene 181 (1-2), 219-220 (1996)		
MEDLINE	97128794		
REFERENCE	2 (bases 1 to 1510)		
AUTHORS	Tsurushita, N.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-MAR-1996) Neoya Tsurushita, Protein Design Labs, Inc., 2375 Garcia Avenue, Mountain View, CA 94043, USA		
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BASE COUNT	467 a 328 c 349 g 366 t		
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Query Match	59.88; Score 1351.2; DB 85; Length 1510;		
Best Local Similarity	95.68; Pred. No. 0;		
Matches 1422; Conservative	0; Mismatches 63; Indels 3; Gaps 3;		
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Qy	221	GGAACCTCTGCTGACTTACCATATTTCTGAAAAACCATGAAGTGGCAAGGACTGA	290
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Qy	351	TATCTGGAAGAGACTCTGGCCCTTTCAGTCGTTCTTACTACTGATAGGAATCCGAAGATA	410
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Qy	411	GGAGGAATATGAGAGCTGGGTGGGAACCAACAATCTCTCATGGAAGACAGAACTGG	470
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Qy	471	GGAGATGCTGAGACCCCAACAACAAGAAGACAGAGACTGCTGAGATCTATATCAAG	530
Db	421	GGAGATGCGGAGACCCCAACAACAAGAAGACAGAGACTGCTGAGATCTATATCAAG	480
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Qy	651	ATCAATTAATCACACCTGCAACTGTGATGTGGGTACTATGAGGCCCACTGACCTTGTG	710
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Qy	771	GGAAACTTCAGCTTCAGCTTCACAGTGTGCTCAGCTGCTCTGGAAGAACAACTTAAT	830
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Qy	831	GGGATTGAAGAAACACCTGTGGACCAATTTGGAACCTGTCTCCAGAACCAACTGT	890
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Qy	891	CAAGGATTCAGTGTGACGCTCTATCACACACAGATTTGGGATCATGAACTGACCT	950
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Qy	951	CCCCTGGGACGCTTCAGCTTACCTCTGATGATCTTCATCTGCTCGAAGGAAGACTGAG	1010
Db	901	CCCCTGGGACGCTTCAGCTTTCCTCTGCTGCTGATCTTCATCTGCTCGAAGGAAGACTGAG	960
Qy	1011	TTAAATGGGAAGAAACCACTTTGTGAATCAGTGAATCTGCTCAAACTCTGATCCA	1070
Db	961	CTAATTTGGGAGAAAGAAACCACTTTGTGAATCAGTGAATCTGCTCAAACTCTGATCCA	1020
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Db	1021	ATATGTCAAAAATTTGGACAAAAAGTTTCTCAATGATTAAGAGAGCTGATTAATACCCCTC	1080
Qy	1131	TTTATTCAGTGGGACGATGATGTTACTGCTCATTTCTGCGTTGGGACTTATATCTTTGGCTG	1190
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Qy	1191	GCAAGGAGATTAAAAAAGGCAAGAAATCCAAGAGAACTATCAATGACCATATTAAATC	1250
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Qy	1311	ATGAACGTTTTGTGTGGTGGACCTCTACGTCAAACATGAAGTGTG-TTCCCTCAGTG	1369
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Qy	1370	CATCTGGGAAGATTTCTACCGGACCAAGAGTTCTTCAAGTTCATTTCCGCCCTCATTTT	1429
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Db 1441 GAAACAAATAAGCCATATAAGGGAAGATTAATGTGGAATACCAAA 1488

RESULT 12  
PTU73728 1119 bp mRNA PRI 05-NOV-1996  
LOCUS Pan troglodytes L-selectin mRNA, complete cds.  
DEFINITION U73728  
ACCESSION 073728.1 GI:1658019  
VERSION  
KEYWORDS  
SOURCE chimpanzee.  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.  
REFERENCE 1 (bases 1 to 1119)  
AUTHORS Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and  
Tsurushita,N.  
TITLE Cloning of the cDNA encoding L-selectin from nonhuman primates  
JOURNAL Unpublished  
2 (bases 1 to 1119)  
REFERENCE Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and  
AUTHORS Tsurushita,N.  
TITLE Direct Submission  
JOURNAL Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia  
Avenue, Mountain View, CA 94043, USA  
FEATURES  
source Location/Qualifiers  
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BASE COUNT 332 a 236 c 277 g 274 t  
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Query Match 48.8%; Score 1101.4; DB 85; Length 1119;  
Best Local Similarity 99.0%; Pred. No. 2.6e-285;  
Matches 1108; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 189 TGGGGGTGACAAATGCTGTGATTTCTGACATCATGGAACCTCTGCTGACT 248  
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RESULT 13  
PPU73729 1119 bp mRNA PRI 05-NOV-1996  
LOCUS Pongo pygmaeus L-selectin mRNA, complete cds.  
DEFINITION U73729  
ACCESSION 073729.1 GI:1658017  
VERSION  
KEYWORDS  
SOURCE orangutan.  
ORGANISM Pongo pygmaeus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pongo.  
REFERENCE 1 (bases 1 to 1119)  
AUTHORS Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
FEATURES  
Source  
CDS  
BASE COUNT  
ORIGIN  
Query Match  
Best Local Similarity  
Matches 1098; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
48.0%; Score 1085.4; DB 85; Length 1119;  
98.1%; Pred. No. 5.2e-281;  
233 c 273 g 277 t

Tsurushita, N.  
Cloning of the cDNA encoding L-selectin from nonhuman primates  
Unpublished  
2 (bases 1 to 1119)  
Budman, J. I., Fu, H., Johnson, C. E., Thakur, A. B., Berg, E. L. and  
Tsurushita, N.  
Direct Submission  
Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia  
Avenue, Mountain View, CA 94043, USA  
Location/Qualifiers  
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LOCUS MMU73730 1119 bp mRNA PRI 05-NOV-1996  
DEFINITION Macaca mulatta L-selectin mRNA, complete cds.  
ACCESSION U73730  
VERSION U73730.1 GI:1658015  
KEYWORDS  
SOURCE  
ORGANISM  
Macaca mulatta.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
Cercopithecoidea; Macaca.  
1 (bases 1 to 1119)  
Budman, J. I., Fu, H., Johnson, C. E., Thakur, A. B., Berg, E. L. and  
Tsurushita, N.  
Cloning of the cDNA encoding L-selectin from nonhuman primates  
Unpublished  
2 (bases 1 to 1119)  
Budman, J. I., Fu, H., Johnson, C. E., Thakur, A. B., Berg, E. L. and  
Tsurushita, N.  
Direct Submission  
Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia  
Avenue, Mountain View, CA 94043, USA  
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Matches 1080; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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DEFINITION Oryctolagus cuniculus L-selectin precursor, mRNA, complete cds.
ACCESSION U26535
VERSION U26535.1 GI:847787
KEYWORDS
SOURCE
ORGANISM
Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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REFERENCE 1 (bases 1 to 1680)

AUTHORS Qian,J. and Marks,R.M.  
TITLE cDNA for rabbit L-selectin  
JOURNAL Unpublished  
AUTHORS Qian,J.  
TITLE 2 (bases 1 to 1680)  
JOURNAL Direct Submission

Submitted (08-MAY-1995) Jin Qian, Internal Medicine, University of Michigan, Kresge I, Rm, 4570, Ann Arbor, MI 48109, USA  
LOCATION/Qualifiers  
1. 1680

FEATURES  
source

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Job time: 18955 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2001, 20:00:14 : Search time 125.58 Seconds  
(without alignments)  
6757.621 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259  
Sequence: 1 GAATTCACAGTGTGCTGGCTT.....CCGCGACGACACTGGAATTC 2259

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	2255.8	99.9	16	092802	Human LHR CDNA. H
4	2255.8	99.9	16	T03003	Human LHR CDNA. H
5	2255.8	99.9	17	T30003	Human lymphocyte c
6	2255.8	99.9	19	V15012	Human lymphocyte c
7	2254.2	99.8	14	043154	Human lymphocyte h
8	2251.8	99.7	12	012118	Sequence encoding
9	2241.6	99.2	13	023623	Human lymphocyte h
10	2241.2	99.2	13	024987	Sequence encoding
11	2127.8	94.2	17	T14723	Human Leu8 antigen
12	2126.2	94.1	13	021184	Encodes T lymphocy

13	2126.2	94.1	2350	19	V63460
14	2126.2	94.1	2350	20	V81217
15	2087.6	92.4	2330	15	071006
16	2086	92.3	2330	14	035142
17	2076.4	91.9	2330	14	038839
18	2076.4	91.9	2330	18	T72270
19	2074.8	91.8	2330	14	037304
20	2058.8	91.1	2327	11	005871
21	2033.4	90.0	2330	13	031767
22	1271.8	56.3	1914	13	025500
23	970.2	42.9	138169	21	A34791
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35	848.8	37.6	2214	12	Q12119
36	828.8	36.7	1496	11	005542
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38	385.2	17.1	531	15	071009
39	385.2	17.1	5866	14	038840
40	383.6	17.0	5564	13	031768
41	310	13.7	2490	19	V16208
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#### ALIGNMENTS

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KM lymphocyte binding; endothelium; graft rejection; inflammation; therapy;	
KW arthritis; autoimmune disease; lymphoma metastasis;	
KW lymphocyte accumulation; human; ss.	
OS Homo sapiens.	
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PN US5840844-A.	
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PD 24-NOV-1998.	
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PF 10-AUG-1995;	95US-0513278.
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PR 23-FEB-1989;	89US-0315015.
PR 31-OCT-1991;	91US-0786149.
PR 06-MAY-1993;	93US-0059029.
PR 10-AUG-1995;	95US-0513278.
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PA (GETH ) GENENTECH INC.	
PA (REGC ) UNIV CALIFORNIA.	
XX	
PL Lasky LA, Rosen SD, Slinger MS, Stachel SE;	
XX	
DR WPI: 1999-034122/03.	
DR P-PSDB; W73264.	

Human Leu8 antigen  
Human Leu8 antigen  
L-selectin CDNA.  
LAM-1 B125 CDNA. c1  
Sequence of LAM-1  
Human lymphocyte-a  
LAM-1 CDNA from PL  
Sequence encoding  
Human LAM-1. Homo  
Encodes T lymphocy  
Human adenosine re  
Human adenosine re  
Lym-1 gene exon X  
Murine lymphocyte  
Sequence encoding  
Murine lymphocyte  
Murine LHR CDNA. M  
Mouse LHR CDNA. M  
Mouse lymphocyte c  
Mouse lymphocyte h  
Sequence encoding  
Sequence encoding  
Mus musculus Lymph  
Lym-1 gene exon I  
Sequence of exons  
Genomic Human LAM-  
CDNA encoding huma  
Human adenosine re  
Cloned sequence en  
CDNA encoding E-9e  
Human ELAM-1 codin



QY 1801 TAGCTGCGCCCTCTGTGAATTGACCATCTATTAACTGGCTTCAGGCTCCACCCTT 1860  
|||||  
Db 1801 tagctgcgcgtcgtgtaattggacacatcctatctaacttgcttcagcctccaccactt 1860  
QY 1861 CTTCAGCCACCTCTCTCTTTTTCAGTTTGGCTGACCTTCACACCTTACATGATGCGCA 1920  
|||||  
Db 1861 cttagcaccctctctcttcttcaagtgtgctgactccacactagatctcatgagtgcca 1920  
QY 1921 AGCAAAAGSAGSAGSAGSAGSAGSAGSAGSAGSAGSAGSAGSAGSAGSAGSAGSAGS 1980  
|||||  
Db 1921 agcaaaaggag 1980  
QY 1981 TTTCTTTTATGAGACCCCTTCTCTATTCTTATGATGATGATGATGATGATGATGATGATG 2040  
|||||  
Db 1981 ttctcttataagagacacatcctatcttcttataagagagagagagagagagagagagag 2040  
QY 2041 TTTAGTAAAGAAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2100  
|||||  
Db 2041 ttagtaagaaacacatcctatcttcttataagagagagagagagagagagagagagagag 2100  
QY 2101 AAGAGTTAAAG 2160  
|||||  
Db 2101 aagagttaaag 2160  
QY 2161 CCCCCAGACCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2220  
|||||  
Db 2161 cccccagacatcttatactcacttacttacttacttacttacttacttacttacttactt 2220  
QY 2221 CTCCCTCAACCCCAAGGCGCGCCGACGACGACGATGCAATTC 2259  
|||||  
Db 2221 ctccctcaaccccaagcgcgccgacgacactggaattc 2259

## RESULT 2

Q44243 standard; DNA; 2259 BP.

Q44243;

11-JAN-1994 (first entry)

HULHR DNA.

Human: murine; lymphocyte; cell surface glycoprotein; homing receptor;

LHR; endothelium; lymphoid tissue; signal; domain; complement binding;

carbohydrate binding; epidermal growth factor-like; egf; intracellular;

transmembrane binding; cytoplasmic; ligand binding partner protein;

TMD; LBPP; ss.

Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo sapiens.

Homo sapiens.

XX WPI: 1993-226664/28.  
DR P-PSDB: R38908.  
XX  
PT New lymphocyte homing receptor immunoglobulin fusion  
PT polypeptide(s) - used to inhibit binding of lymphocytes in  
PT therapeutic and diagnostic uses  
XX  
PS Disclosure: Fig 1: 44pp: English.  
XX  
CC The sequences given in Q44243-44 encode human and murine lymphocyte  
CC cell surface glycoprotein (LHR) respectively. The proteins encoded  
CC by these sequences mediate the binding of lymphocytes to the  
CC endothelium of lymphoid tissue. LHR is a glycoprotein which contains  
CC a signal domain, a carbohydrate binding domain, an epidermal growth  
CC factor-like (egf) domain, at least one complement binding domain  
CC repeat, a transmembrane binding domain (TMD) and a charged intra-  
CC cellular or cytoplasmic domain. The murine and human amino acid  
CC sequences show a high degree of overall homology (83%), however  
CC degrees of homology between the various domains is variable. These  
CC proteins may be fused to a ligand binding partner protein (LBPP) which  
CC causes an increase in the half life of the LHR. The fusions may be  
CC used therapeutically to compete with the normal binding of  
CC lymphocytes to lymphoid tissue. They may be used in organ or graft  
CC rejection and for the treatment of inflammation.  
CC  
XX  
SQ Sequence 2259 BP: 635 A; 516 C; 489 G; 619 T; 0 other:

Query Match 99.94; Score 2255.8; DB 14; Length 2259;  
Best Local Similarity 99.94; Pred. No. 0;  
Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAATTCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60  
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Db 1 gaattcgaagtgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 60  
QY 61 GAGACCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
|||||  
Db 61 gagacctttgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 120  
QY 121 GCAAGCCATGATATTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 180  
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Db 121 gcaagccatgatatttttcattgataatgataatgataatgataatgataatgataatgataat 180  
QY 181 TCAAGTTGTGGGGTGGGAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
|||||  
Db 181 tcaagttgtggggtgggagcattgctgctgctgctgctgctgctgctgctgctgctgctgct 240  
QY 241 GCTGACCTTACCATTTATTTTCAAAACCAGTGAAGAGGCTTGAAGATTTGCTGCTGCTGCTG 300  
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Db 241 gctgaccttaccatttatttctgataaaaccagagagagagagagagagagagagagagagag 300  
QY 301 GAGACATTTACAGATTTTATTTTGCATATCAAAACAGCGGAAATTTGATATCTGAGAGA 360  
|||||  
Db 301 gagacatttacagatttttatttgcattataaaacagcggaatttgatctcggaga 360  
QY 361 AGACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
|||||  
Db 361 agactgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 420  
QY 421 GGACGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
|||||  
Db 421 ggaagtgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 480  
QY 481 AGCCCAACACAG 540  
|||||  
Db 481 agcccaacacag 540  
QY 541 ATGCAAGCAATGAG 600  
|||||  
Db 541 atgcagcaaatgag 600

[illegible]

Db	1681	ttctgtatactatcgtggaaggtgaacctcttataagaagaattcaaaaaagcttaagctctcttc	1740
Qy	1741	TTTTCTTACTCCAGTGAAGTAATGGGGTCCGTGCATGTTGAAGAAGTCCATTATTTGCACTG	1800
Db	1741	ttcttaacctcagatgaatgaatgaggtccctgtctcaagttgaagaagctctatttgcactg	1800
Qy	1801	TAGCCTCGCGCTGTGGAATTTGGACCAATCCATTATTAAGTGGCTTCAGGCTCCGCCACCTT	1860
Db	1801	tagctctgcgcgtctgtgaattgagccacccatttaacttgcctcaggtccctccaccctt	1860
Qy	1861	CTTCAAGCCACTCTCTCTTTTTCAGTTGAGTGGCTGAATTCCACACCCTAGCAATCTCATAGTGCCA	1920
Db	1861	cttcagccaccctctcttlltcaagttgctgacttccacaacctagcaltctcatlgaagtgcga	1920
Qy	1921	AGCAAAAGAGAGAGAGAGAAATATAGCTGCGCGGTTTTTTTACGTTGGGGGTTTGGCTGT	1980
Db	1921	agcaaaagagagagagagaataagcctgcgcggtlltlltlaagtttgggggttttgcgtg	1980
Qy	1981	TTCCCTTTTATAGAGCCACTTCATTTCTATTCTTATGCAATGTTCTTTTATCAGAGATTTA	2040
Db	1981	ttccctttatgagagccacttctctattctctatagtcacatgttctcttcttaccagacatta	2040
Qy	2041	TTAGTAAGAAAACATCACTGAATGCTAGTGCATGCAAGTGACATCTCTTTGATGTGATATAGG	2100
Db	2041	ttagtaagaaaacatcaatgaatgctagctgcgaagtgacatctcttgaatgctacataag	2100
Qy	2101	AAGAGTTAAACACAGGTGAGAAATTCCTTGATTCACAAATGCAATGCTCTCTTTCCCTTG	2160
Db	2101	aagagttcaaaacaggtgagaaattccttgatcttcaacaagaatgctctcttccccg	2160
Qy	2161	CCCCCAGAACTTTTATCCACTTACCTAGATTCTACATATTTCTTTAAATTTTCATCTGAGG	2220
Db	2161	cccccaagaactttatccacttaactagatctcaacatattctttaattcattcccaagc	2220
Qy	2221	CTCCCTCAACCCACGSGGGCCGCGACACACTGGAATTC	2259
Db	2221	ctccctcaacccacagggcgccagacactlgaattc	2259
RESULT 3			
ID	Q92802	standard; CDNA; 2259 BP.	
XX	Q92802;		
AC	01-DEC-1995	(first entry)	
XX			
DT			
XX			
DE	Human LHR CDNA.		
XX			
KW	Lymphocyte homing receptor; lymphocyte cell surface glycoprotein;		
KW	LHR; ligand binding partner; immunoglobulin; constant region;		
KW	antibody engineering; immunomodulator; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	129..1247	
FT		/*tag= a	
FT	sig_peptide	186..224	
FT		/*tag= b	
FT	mat_peptide	243..1244	
FT		/*tag= c	
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PN	US5428130-A.		
XX			
PD	27-JUN-1995.		
XX			
PF	23-FEB-1989;	89US-0315015.	
PR	22-NOV-1989;	89US-0440625.	
PR	23-FEB-1989;	89US-0315015.	
PR	16-DEC-1991;	91US-0808122.	



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D 1801 tagctcgccgctcgtgatgagccatccatttaactagctcagcgctccccaactt 1860
QY 1861 CTTGAGCCACTCTCTTTTTCAGTTGGCTGACTTCCACACCTTAGCATTCATGAGTCCCA 1920
D 1861 cttaagccactctcttcttaagcttgagcttccacactagcatcatgagtgcca 1920
QY 1921 AGCAAAAGAGAGAGAGAGAAATAGCCTGCGCGTCTTTTACCTGGGGCTTTTGGCTGT 1980
D 1921 agcaaaagagagagagagagaaatagcctcgcggttttcttaagcttgaggggttctgt 1980
QY 1981 TTCTTTTATGAGACCATTCCTATTCTTTATATGTCAAATGTTCTTTTATCAGATATTA 2040
D 1981 ttcttcttaagagaccatctctattcttataagtaagttcttcttatacaagatatta 2040
QY 2041 TTGTAGAAACATCATCTGAATTCAGTGTGCAAGTGTGCAATCTCTTTGATGTCAATGG 2100
D 2041 ttgtagaagaaacatcatctgaatctagctgtagctgcaagtgacatctcttgatgtcata 2100
QY 2101 AAGAGTTAAACAGGTGAGAAATTCCTTGATTCACATGAATGCTCTTCCTTTCCCTTG 2160
D 2101 aagagttaaacaagtgtaggaatctcttgatccacaatgaatgctctccttcccttg 2160
QY 2161 CCCCCGAACTTTTATCCACTTACCTAGATTCATATTTCTTTAAATTCATCTCAGGC 2220
D 2161 cccccgaacttcttacccttaacttaccatagattctacatattctttaaattctcaagc 2220
QY 2221 CTCCTTCACACCCCGCGGCGCCGACGACACATGGAATTC 2259
D 2221 ctccctcaaccccgcgggcgccgacacatcggaattc 2259

RESULT 4
T05869 standard; cDNA: 2259 BP.
XX T05869:
AC T05869:
XX
XX 31-JAN-1996 (first entry)
XX
DE Human LHR cDNA.
XX
XX Lymphocyte cell surface glycoprotein; LHR; transmembrane receptor;
XX immunoglobulin; IgG; constant region; receptor-mediated disease;
XX vector; plasma-11fe; ss.
XX
OS Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 129..1247
XX FT /*tag= a
XX FT sig_peptide 186..224
XX FT mat_peptide 243..1244
XX FT /*tag= b
XX FT /*tag= c
XX FT /product= LHR
XX
XX US5455165-A.
XX
XX
XX 03-OCT-1995.
XX
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185669.
XX
XX (GENE ) GENENTECH INC.
XX Capon DJ, Lasky LA;
PI
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XX
DR WPI: 1995-350776/45.
DR P-PSDB: R83050.
XX
XX Expression vector encoding fusion protein to increase plasma life-
XX comprises receptor ligand binding site and Ig constant region, for
XX treatment of receptor mediated disease
XX
XX Disclosure: Fig 1; 42pp; English.
XX
XX A mouse LHR (lymphocyte cell surface glycoprotein) cDNA clone was used
XX to screen an oligo-dT primed lambda gt10 cDNA library derived from
XX human peripheral blood lymphocyte mRNA obtd. from primary cells. A
XX 2.2 kb clone (sequence given in T05869) showing 83% DNA sequence
XX homology to the murine LHR gene (T05870) was isolated. The LHR genes
XX are used to construct LHR-IgG hybrids used to target therapeutic
XX moieties to lymphoid tissue.
XX
SQ Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

Query Match 99.9%; Score 2255.8; DB 16; Length 2259;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAATTCGAGTGTGGTGGCTTCTCACCAGCAGCAGCAGCATCTCCCTTGGCAAGACT 60
D 1 gaattcgaagtggtgggtcttctcaccagcagcagcagcatctcccttggcaagact 60
QY 61 GAGACCCCTTGTGCTAAGTCAAGAGGCTCAATGGGCTGCAGAGAACTAGAGAGGCCAA 120
D 61 gagaccccttgtgctaaagtcaagaggtcgaatgggctgcagagaaactagaagaagccaa 120
QY 121 GCAAGCCATGATATTTCATGGAATGTCAGAGACCCAGAGGACTTATGGAACATCT 180
D 121 gcaagccatgatatttcgatggaatgtcagagacccagagacttataggaacatct 180
QY 181 TCAAGTTGTGGGGGTGAGCAATGCTGTGTGATTTCCGGGCAATCAATGGAACCTACT 240
D 181 tcaagttgtgggggtgagcaatgctgtgtgatttccgggcaatcaatggaaacctact 240
QY 241 GCTGGAATTAACATTAATTTGAAAAACCATGAACTGGCAAGGGCTAGAAATTTGCGC 300
D 241 gctggaattaacattaatTTTgaaaaacccatgaaactggcaagggttagaatttcgccc 300
QY 301 GAGCAATTTACAGAAATTTAGTCCATACAAACAGCGGGAATTTGATCTTGAGAGA 360
D 301 gagcaattttacagaaTTTtagtccatACAAACAGCGGGAATTTgattcttgagaga 360
QY 361 AGACTGCCCCCTCAGTCTGTTTACTAGTAGAATTCGGAATGATGAGGAAATAT 420
D 361 agactgccccctcagTCTgTTTactAGTAGAATTCGGAATGATgaggaatagagaatatt 420
QY 421 GGAAGTGGGTGGGAGAACCAACAAATCTCTACTGAGAGACAGAGAACTGGGAGATGGTG 480
D 421 ggaagtgggtgggagAACCAACAAATCTCTactGAGAGACAGAGAACTGGGagatggtg 480
QY 481 AGCCAAACAAGAGAGACAAGAGAGACTGGGTGAGATCTATATCAAGAAACAAG 540
D 481 agccaaacaagAGAGACAAGAGAGACTGGGTGAGATCTATATCAAGAAACAAG 540
QY 541 ATGCAAGCAAAATGAGATGATGAGCGCTGCGACAACTAAAGCAGCCCTGTTACACAG 600
D 541 atgcaagcaaaATGAGATGATGAGCGCTGCGACAACTAAAGCAGCCCTgtttacacag 600
QY 601 CTTCTTGCAAGCGCTGGTATGCAATGGCATGGCATGATGTGTAATATCAATCAATATC 660
D 601 ctctcttgcaagCGCTGGTATGCAATGGCATGGCATGATGTGTAATATCAATCAATATC 660
QY 661 ACACCTGCAACTGTATGTGGGTACTATGGGCCAGCTGACGTTGTGATTCAGTGTG 720
D 661 acacctgcaactgtatGTGGGTACTATGGGCCAGCTGACGTTGTGATTCAGTGTG 720
```



QY 721 AGCTTTGGAGGCCCGAGAGCTGGGTACCATGAGCTGACTACACCCCTTTGGAACTTCA 780  
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 Db 721 agccttggagggcccccagagctgggtaccagtgactgtactcaacccttggaaacttca 780  
 QY 781 GCTTCAGCTCAGAGTGTGCTTTACAGCTCTCTCTCAAGAACAACTTAACCTGGATTGAAG 840  
 |||||||  
 Db 781 gcttcagctcagagtgctctcagctgctcgtgaaggaacaacttaacttgatgag 840  
 QY 841 AAACACCTGTGAGACATTTTGGAAACGTGTCTCCAGAACCAACGTCAAGGATATTC 900  
 |||||||  
 Db 841 aaacacacctgtgagacatttggaaacctgtgtcaatcccaagaacaacctgtcaagtgtatc 900  
 QY 901 AGTGTGACCTCTATTCACAGCACCAGATTTTGGGATCATGAGCTGATGCCATCCCTGGCCA 960  
 |||||||  
 Db 901 agtgtgagccctctatcagcaccaagcttgggatcatgaactgtgacatccctggcca 960  
 QY 961 GCTTCAGCTTTACCTCTCTCATGTGTACCTTTCATCTGCTCAGAAAGGAATCAGTTAATGGGA 1020  
 |||||||  
 Db 961 gcttcagcttcaacctgtgacatctcctcatctgctcagaagaacttgatlaatlgsa 1020  
 QY 1021 AGAGAAACCAATTTGTGAATCATCTGGAATCTGGTAAATCTGATCCATATATGTCAAA 1080  
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 Db 1021 agagaaacaaacctgtgtgaatcatctggaaacctgggtcaaatccctagttccaatlatgtcsaa 1080  
 QY 1081 AATTGGACAAAAGTTTCTCAATGATTTAAGGAGGTGATTTAAACCCCTCTTCATTCAG 1140  
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 Db 1081 aattggacaaaagtttctcaatgatttaaggaggtgattataaaccccttctcatctcag 1140  
 QY 1141 TGGCAGTCATGTGTTACTGCATTTCTCTGGGTTGGCATTTATCATTTTGGCTGGCAAGGAGAT 1200  
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 Db 1141 tggcagtcatgtgttactgcatttctctgggttggcatttatcatatttggctggcaaggagat 1200  
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 Db 1381 atttcctaccgaccaaagcttccctcagcttccatcttcgcccctcaattatccctcaacc 1440  
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 Db 1501 gaccataagggaaagatcatctgtgaatataaagaatggcgtgacttgcctcttcttgac 1560  
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 Db 1741 ttctctaactccagtgaagtaatgggtctctctcaagttgaaagagttcttcttctgacatg 1800  
 QY 1801 TAGCTCGCGTGTGTGAATTTGAGCAATCTATTTTAACTGGCTTCAGGCTCCCACTT 1860

Db 1801 tagctcgcgctgtgtgaatltvgaccatccatcttaactggtctcagggccctcccaactt 1860  
 QY 1861 CTTCAGCCACCTCTCTTTTTCAGTTTGGCTGACTTTCACACCTCAGATCTCATGATGCCA 1920  
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 Db 1861 cttcagccacctctcttcttctcagltggtcgtacatccacacatgcatctcagatgagtgcca 1920  
 QY 1921 AGCAAAAGAGAGAGAGAAATAGCCTGGCGGTTTGTATGTTTGGGGTTTGTGCTGT 1980  
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 Db 1921 agcaaaagagagagagagaaatagcctggcggtcttctttagttcttgggggttctgcgtg 1980  
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 Db 2041 ttagtaagaagaaacatcacatgaaatgctgtgcaagtgacatctctctgtgacatglatg 2100  
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 Db 2101 aagagttaaacaggtggagaaatctcctgtatccacaaatgaaatgcttcccttccctg 2160  
 QY 2161 CCCCCAGAACTTTTATTCACATTCCTAGATTCATATTCCTTTAAATTTGATCTCAGGC 2220  
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 Db 2161 cccccagaaactttaaactcacatctacatagatctctacatattcttcttcttcaatctcagagc 2220  
 QY 2221 CTCCCTCAACCCCGACGGGCGCCGACGACACTGTGCAATTC 2259  
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 Db 2221 ctccctcaaccccgacgggcccgcagcacactggaatctc 2259

RESULT 5  
 T30003  
 ID T30003 standard; DNA: 2259 BP.  
 XX  
 AC T30003:  
 XX  
 DT 31-Oct-1996 (first entry)  
 XX  
 DE Human lymphocyte cell surface glycoprotein (HULHR) coding sequence.  
 XX  
 KW Immunoglobulin; transmembrane receptor; adhesion; targeting;  
 KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;  
 KW immunomodulator; cell adhesion; graft rejection; inflammation;  
 KW metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 129..1247  
 FT sig\_peptide /tag= a  
 FT mat\_peptide /product= Lymphocyte cell surface glycoprotein.  
 FT /tag= b  
 FT /tag= 129..242  
 FT /tag= 243..1244  
 FT /tag= c  
 PN US5514582-A.  
 PN  
 PD 07-MAY-1996.  
 PD  
 PE 23-FEB-1989; 89US-0315015.  
 PE  
 PR 22-NOV-1989; 89US-0440625.  
 PR 23-FEB-1989; 89US-0315015.  
 PR 16-DEC-1991; 91US-0808122.  
 PR 08-DEC-1992; 92US-0986931.  
 PR 21-JAN-1994; 94US-0185670.  
 PA (GENTECH ) GENENTECH INC.  
 PI Capon DJ, Lasky LA.

XX WP1: 1996-238773/24.  
DR P-PSDB: R98106.  
XX  
PT Nucleic acid encoding hybrid immunoglobulin comprising the ligand  
PR binding site of a receptor fused to Ig constant region - useful for  
PR diagnosis and treatment e.g. of inflammation  
XX  
PS Example 2; Figure 1; 41pp: English.  
XX  
CC A hybrid immunoglobulin chain comprising the ligand binding site of  
CC a single transmembrane receptor without an active transmembrane  
CC region; fused at its C-terminus with the N-terminus of an  
CC immunoglobulin constant region. The receptor is not a member of the  
CC immunoglobulin super family, nor a multiple subunit polypeptide  
CC encoded by discrete genes. The hybrid immunoglobulin chain combines  
CC the adhesion/targeting of a ligand binding partner (LBP) with the  
CC effector functions of immunoglobulin and can bind to and/or activate  
CC more than one ligand. It can be used diagnostically for the in  
CC vitro assay of LBP and their targets; or therapeutically to deliver  
CC LBP such as toxins, enzymes, growth factors to particular cells.  
CC Typical applications are as antiviral, neuromodulating and  
CC immunomodulating agents, or as modulators of cell adhesion (e.g. in  
CC treating graft rejection, inflammation; metastasis of lymphoma etc.)  
CC The immunoglobulin component increases plasma half life and  
CC facilitates purification while deletion of the transmembrane region  
CC potentially improves aqueous solubility and removes  
CC potentially immunogenic epitopes.  
XX  
SQ Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other:  
  
Query Match 99.9%; Score 2255.8; DB 17; Length 2259;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2257; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 GAATTCAGTGTGCTGCTGCTCCTCCACCTGACAGACACATCCCTTGGCAAGGACT 60  
DB 1 gaattccagtgctgctgctcctccacgacagacacatccttctgcaaaagact 60  
QY 61 GAGACCCCTGTGCTAAGTCAAGAGGCTCAATGGGCTGCAGAAAGACTAGAGAGCCAA 120  
DB 61 gagaccctgtgtctaagtcagaagagctcaatggtctgcagaagaactagagaagccaa 120  
QY 121 GCAAAGCCATGATATTTCCATGAGAAATGTCAGAGACCCAGAGGACTTATGGAACATCT 180  
DB 121 gcaaaagccatgatattttccatgagaaatgtcagagacccagagagacttataggaacatct 180  
QY 181 TCAAGCTTGGGGGTGACAAATGCTGCTGTTGATTTCTGGCAGCATGGAAGCACTACT 240  
DB 181 tcaagcttgggggtgacaaatgctgctgctgattttctggcagcatggaagcaactact 240  
QY 241 GCTGCACTTACCATTTATCTGAAAAAACCAGTGAACCTGGCAAAAGGCTTAGAATTCTGCC 300  
DB 241 gctgcacttaccatttatctgaaaaaaccagtgaaactgycaaaggcttagaagattctgcc 300  
QY 301 GAGACAATTACAGAGATTAGTGCATACAAACAAGGGGGAATGAGATATGAGAGA 360  
DB 301 gagacaattacagagatttagtgcatacaaaacaaggcggaatgagataltcgaaga 360  
QY 361 AGACTTCGCTTCAGTGTCTTACTACTAGATAGGAATCCGGAAGATAGAGGAATAT 420  
DB 361 agacttcgcttccagtcgttcttactactcgtatagaatccggaagatagagggaatat 420  
QY 421 GGAGTGGGTGGGGAACAACAATCTCTCACTGAAGAGCAAGAACTGGGGAGATGCTG 480  
DB 421 ggaagtgggtggggaacaacaatctctcactgaagagcaagaaactggggagatgctg 480  
QY 481 AGCCCAACAACAAGAAAGCAAGAGAGACTGCGTGGAGATCTATACAGAGAGAAACAAG 540  
DB 481 agcccaacaacaagaaagcaagagagactgctggagatctatatacaagaagaaacaag 540  
QY 541 ATGCAGGCAATGAGAGATGACGCTCCACAAACTAAAGGCGCCCTCTGTACACAG 600

DB 541 atgcaggaacaatggaacgatgacgcctgcacaacaactaaaggccctctgttaccag 600  
QY 601 CTTCCTGGCCAGCCCTGGTGCATGCTAGTGGCCATGGAGAAATGTGTAGAAATCATATATC 660  
DB 601 ctctctggccagccctgggtgcattgctagtgccatggagaaatgtgtagaaatcatac 660  
QY 661 ACACCTGCAACTGTGATGGGGTACTATGGGCCCCAGTGTACACTTGTGATGACTGTG 720  
DB 661 acaactgcaactgtgatggggactatgggccccagtgctgactgtatcaagtgtg 720  
QY 721 AGCCCTTGGAGGCCCCCAAGCTGGGTACCATGACTGACTACTACCCCTTGGAAACTCA 780  
DB 721 agcccttggagggccccagagctgggtacacatgactgactaccccttggaaactca 780  
QY 781 GCTTCAGCTCAGATGTGCTTCAGCTGCTGTGAAGAACAACTTATACCTGGGATGGAAG 840  
DB 781 gcttcagctcagatgtgcttcagctgctgtgaagaaaccttattacctgggattggaag 840  
QY 841 AACACCTGTGGACACATTTGGAAACTGTTCATCTCCAGAACCCCTGTCAAGTATTTC 900  
DB 841 aaacacctgtggacacatttggaaactgttcattctccagaaacctgtcaagtgatttc 900  
QY 901 AGTGGACCTCTATTCAGACACCAATTTGGGGAATCAGAACTGTACCATCCCTGGCCA 960  
DB 901 agtggacctctatctcagaccagatctggggaatcagaaactgtacatgcccttggcca 960  
QY 961 GCTTCACCTTTACCTCTGCATGATACCTTCACTGCTCAGAAAGAACTGATTAATTTGGA 1020  
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DB 1261 aaagaaatttcttggaaatctaaaaatcatgagatctttaatcccttcatactgaagagtt 1320  
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DB 1321 ttgctgtgggtggacctccagagtcaaaacatgaagtgtcttctcctaagtgatcctgggaag 1380  
QY 1381 ATTTCACCCGCAACAAGATTTCAGCTTCATTTGCCCCATTTATTCCTCCAGC 1440  
DB 1381 atttcacccgcaacaagatttcagcttcatttcagcttcacatcttgcctccatlaaccctcaacc 1440  
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DB 1501 gaccattaaagggaagagatttcattgtgaattataaagatgggctgatttgccttcttgac 1560  
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DB 1561 tcttgttcttcaagttcaattgagctgtactgtatgaacagaaactcttaaaagagtg 1620  
QY 1621 AAATTGATACATATGGAATATGAGACTGAGTTTCTTGCAGATCAAAATTTCAAGTGTGC 1680



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Db 541 atcgagcgaataggaagatgacgctgcacaaactaaagcagccctgtctacacag 600
QY 601 CTCTTGGCCAGCCCTGGTCATGCAGTGGCCATGAGAAATGTAGAAATCAATCAATATC 660
Db 601 ctctctgcagccctgtctacatgacgctgcacaaactaaagcagccctgtctacacag 660
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Db 661 acacccgcaactgtgattggtgtactatgcgcccagctgtcagctgtgtatcagctgtg 720
QY 721 AGCCTTGGAGGCCCAAGGCTGGGTACAGTGCAGTGTGATTCAGTGTGATTCAGTGTG 780
Db 721 agccttggagggcccaagcctgggtacacatgacgtgtcacccttggaaacttga 780
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Db 781 gcttaccgcaacagctgtcctcagctgtcctgaaggacaaacttaactgtgtatcag 840
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Db 1081 aattgagcaaaaagtcttcccaatgattaaaggggtgtatataacccctcttccatccag 1140
QY 1141 TGGCAGTATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTG 1200
Db 1141 tggcagatgtgtactgtactgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200
QY 1201 TAAAAAAGGAGAAATCCAGAGAGTATGATGATGATGATGATGATGATGATGATGATG 1260
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Db 1441 cccagcccaagagtgattatacagctcatttcttcttcttcttcttcttcttcttcttct 1500
QY 1501 GACCATAGGGAAGGATTTATGTGTGAATTAAGATGGCTGACTTGTCTTCTTGTGAC 1560
Db 1501 gaccataagggaaggaatcatgtgaaataaagatggtgtccttcttcttcttcttcttct 1560
QY 1561 TCTGTGTGTAGTTTCAATTCAGTGTGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1561 tctgtgtgttagtttcaattcagtgctgtactgtatgacagacacacttcaaatgaagtgc 1620
QY 1621 AAATTTGATACATATGTGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1680

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Db 1681 ttctgtatatactgtgaaagttacacctctatagaagaagttcaaaagctcagctctctct 1740
QY 1741 TTTCTAATCTCAGTAAGTATGGGGTCTGCTCTCAAGTTGAAAGAGTCTTATTTGCACTG 1800
Db 1741 ttcttaactccagtgaaatlaaagggtctcgtcctaagttgaagagttccatttgcactg 1800
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Db 1801 tagcctcgcgctgtgtgaatttgacacatctctatctaactgtctcagcctcccccact 1860
QY 1861 CTTACGACCTCTCTTTTTCAGTTGGCTCACTTCACACCTAGACATCTCATGAGTGCCA 1920
Db 1861 cttaagcacctctcttcttcaatgtgctgtgacttccacacactagcatcctaagtgcca 1920
QY 1921 AGCAAAAGAGAGAGAGAGAAATAGCCTGCGGGGTTTTTACTTTGGGGGTTTTCTGT 1980
Db 1921 agcaaaaagagagagagagaaataagcctgcggttctttagtttgggggttttgcgt 1980
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QY 2041 TTATAGAAAGAAATCATCTAATAATGCTAGTGCAGTGCATCTCTTGTGATGATGATG 2100
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QY 2101 AAGAGTTAAACAGGTGAGAGAAATTCCTTGATTTCAACAAGAAATGCTCTTCCCTCCG 2160
Db 2101 aagagttaaacacggtgagagaaatctcttcttcttcaacaagaaatgctctccctccct 2160
QY 2161 CCCCCAGAACTTTTATTCACCTTACTAGATTTCTACATTTCTTAAATTCATCTCAGGC 2220
Db 2161 cccccagaaacttttataccacttaccctagatctcacatcttcaaatcttcaatctccag 2220
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Db 2221 ctccctctcaaccccgaggcgccgacgacacatcgaaatc 2259

RESULT 7
Q43154
ID Q43154 standard; cDNM: 2259 BP.
XX
AC Q43154;
XX
DT 08-OCT-1993 (first entry)
XX
DE Human Lymphocyte Homing Receptor coding sequence.
XX
KW HuLHR; lymphocyte binding inhibition; lymphoma metastasis;
KW transplant rejection; ss.
XX
OS Homo sapiens.
XX
FH Key
FT CDS 129..1247 Location/Qualifiers
FT FT /*tag= a
FT FT /product= HuLHR
FT FT sig_peptide 186..224
FT FT /*tag= b
XX
PM US5216131-A.
XX
PD 01-JUN-1993.
XX
PF 23-FEB-1989; 89US-0315015.
XX
PR 23-FEB-1989; 89US-0315015.
PR 31-OCT-1991; 91US-0786149.

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XX (GETH ) GENENTECH INC.  
XX  
XX Lasky LA, Rosen SD, Singer MS, Stachel SE, Yednock TA;  
XX WPI: 1993-188588/23.  
XX P-PSDB: R37960.  
XX  
XX Human and murine lymphocyte homing receptors to treat graft  
XX rejection and inflammation - comprise carbohydrate binding,  
XX epidermal growth factor and complement binding domains  
XX  
XX Example 2; Fig 1; 32pp; English.  
XX  
XX A human peripheral blood lymphocyte cDNA library in lambda gt10 was  
XX screened with a 2.2kb EcoRI insert of the murine Me11a antigen clone  
XX (i.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was  
XX isolated and sequenced. The ORF codes for 372 amino acids with a mol.  
XX wt. of approximately 42,200. Comparison of the HuLHR cDNA with the  
XX previously determined murine LHR sequence (Q43155) showed 83%  
XX homology.  
XX  
XX  
XX Sequence 2259 BP; 635 A; 515 C; 490 G; 619 T; 0 other:  
SQ  
Query Match 99.8%; Score 2254.2; DB 14; Length 2259;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2256; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 1 GAATTCAGTGTGCTGGCTTCTCAGCTGACGACAGACACTCCCTTGGCMAAGGACT 60  
DB 1 gaattcagtgctgcttcctccaccctgcagcacagcacactccttggcaagagact 60  
OY 61 GAGACCCCTTGTCGTAAGTCAGAGAGGCTCAATGGCTGCAGAAAGCTAGAGAGACC 120  
DB 61 gagacccttgcgtcaagtcgaagagcctcaatggtcgcagaagaactcgaagaagacaa 120  
OY 121 GCACACCATATATTTTCATGAAATGTCAGAGCACCAGCGAGGACTTATGGAACATCT 180  
DB 121 gcaaaccatatatttccatgaaatgtcagagcaccagcgaagagactcctatggaacatct 180  
OY 181 TCAAGTTGTGGGGGTGACAAATGCTGTGTGATTTCTGGCAGCATGGAACCTACT 240  
DB 181 tcaagttgtgggggtgacaaatgctgtgtgatcttggcagcatggaacctact 240  
OY 241 GCTGAGCTTACCATTTATCTGAAAAACCCATGAACTGGCAAGGGCTAGAGATTCTCC 300  
DB 241 gctgagcttaccatcttctgaaaaacccatgaaactggcaagggctagagattctcc 300  
OY 301 GAGACAATTACAGATTATTTGCTGATACAAACAAAGCGGAAATTAGTATCTGAGAG 360  
DB 301 gagacaattacagattatttgcctgatacaaaacaaagcggaattagatctgagaga 360  
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DB 361 agacttgtcccttaccagtcgtcttactactgatalagaaatccggaaagtagaagaatalat 420  
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DB 421 ggaggtgggtggcaacaataatctctacctgaaagagcagagaactggggagatggtg 480  
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DB 541 atgacaggcaaaatgagagatgagcgctgcgcaaaactaaagcagccctctgttacacag 600  
OY 601 CTTCCTGGCACCCCTGGTGCATGACATGGCCATGGAAGATGTGTAGAATCATCAATATTC 660  
DB 601 ctctctggcacccctgggtgcattgacatggccatgggaagatgtgtagaatcatcaatattc 660

OY 661 ACACCTGCNAAGTGTATGTGGGTACTATAGGCCCCAGTGTGAGCTGTGATTCAGTGTG 720  
DB 661 aaacctgcnaagtgtatgtgggtactatagggccccagtgtgagctgtgattcagtg 720  
OY 721 ACCCTTTGGAGGCCCCAGAGCTGGGTACCAGTGTACTACCCCTTTGGAAACTTCA 780  
DB 721 accctttggaggcccccagagctgggtaccagtgtactacccctttggaacttca 780  
OY 781 GCTTCAGCTCAGAGTGTGCTTCAGCTGCTCTGAAGAGAAACTTAACCTGGGATTTGAAG 840  
DB 781 gcttcagctcagagtgtgcttcagctgctctgaagagaaacttaacctgggattgag 840  
OY 841 AAACCACTGTGAGACATTTGGAACTGATCTCCAGAACCAACGATCAAGTGAATTC 900  
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DB 1021 agaagaaaccatttgtgaatcatctggaatctgctcaaaatctgtcattatattgtcana 1080  
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DB 1081 aattggacaaaagttttcatatgattttaagagaggtgatataatccccctcttcatccag 1140  
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DB 1261 aaagaaaatfttcttggaaatctaaaaatcatgagatcttttaattcccttcagaaagct 1320  
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DB 1621 aaatttgatcatatgttaatatgagactcagtttcttcttcgagatcaaaatttcagctg 1680  
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Db 1741 ttcttaactccagtgagtaatgaggtccctcccaagltgaaagagtcctattgcaactg 1800  
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Db 1801 tagctcgcgcgtctgtaattggaacatcctatttaacgtgtccagccctccacctt 1860  
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RESULT 8  
Q12118  
ID Q12118 standard; DNA: 2259 BP.

AC Q12118;

DT 09-SEP-1991 (first entry)

DE Sequence encoding human lymphocyte cell surface glycoprotein (LHR).

KW Ligand binding partner; lbp; stable plasma protein; spp; antiviral;  
immunomodulatory; neuromodulatory; receptor mediated abnormality; ds.

OS Homo sapiens.

XX Key Location/Qualifiers  
FH 129..1247  
FT /\*tag= a

FT sig\_peptide 186..224

FT /\*tag= b 243..1244

FT mat\_peptide /\*tag= c

XX W09108298-A.

XX 13-JUN-1991.

XX 21-NOV-1990; 90WO-US06849.

XX 22-NOV-1989; 89US-0444625.

XX (GETH ) GENENTECH INC.

XX Capon DJ, Lasky LA;

XX WPI; 1991-193202/26.

XX P-PDB; R12469.

XX New hybrid immunoglobulin(s) - for use as diagnostic reagents for  
PT ligand binding molecules and to treat organ and graft rejection  
PT and inflammation.  
XX  
PS Disclosure; Fig 1; 67pp; English.  
XX  
CC The gene product may be used as a ligand binding partner in combina-  
CC tion with a stable plasma protein eg. IgG1-IgG4, IgA, IgE, IgD or IgM.  
CC The fusion product is joined by N- or C-terminal groups, preferably  
CC the N-terminal of the FC region of the spp is linked to the C-terminal  
CC of lbp. They may be used to provide antiviral, immunomodulatory  
CC and neuromodulatory treatment as well as in treatment of receptor  
CC mediated abnormalities.  
XX  
SQ Sequence 2259 BP; 634 A; 516 C; 487 G; 618 T; 4 other;

Query Match 99.7%; Score 2251.8; DB 12; Length 2259;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2253; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GAATTCAGTGTGCTGGCTTCTCAGTCGACGACACACACTTCCTTGGCAGAGACT 60  
Db 1 gaattccagltgctggcttctcagtcgacgacacacacttccttggcagagacct 60  
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Db 61 gagaccttgtgtaagtcaagagggctgcattgggctgcagaaactagagagaccaa 120  
QY 121 GCAAGCCATGATATTTTCATGGAATGTGAGAGACCCGAGAGGACTTATGGAATCT 180  
Db 121 gcaagccatgatattttcatggaaatgtgagagacccgagagggacttatggaaatct 180  
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Db 181 tcaagttgtggggtgacaaatgctgtgtgatTTCTGGACATCATGAACTACT 240  
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Db 241 gctgacttacCATTTATTTGAAAAACCCATGAACTGAGCAAGGCGTATGAAATCTGCC 300  
QY 301 GAGACAATTACAGAGATTTAGTTGCCATACAAACAGGCGGAATTTGATTTGGAGA 360  
Db 301 gagacaattacagagatTTAGTTGCCATACAAACAGGCGGAATTTGATTTGGAGA 360  
QY 361 AGACTCTGCCCTTCACTGCTTCTTACTAGATAGGAATCCGGAAGATVAGAGAAATAT 420  
Db 361 agactctgcccttcactgcttcttactagataggaatccggaaagatagaagaatat 420  
QY 421 GGAGCTGGGTGGGAAACAATAATCTCTACGTGAAGACGAGAACTGGGGAGATGGTG 480  
Db 421 ggagctgggtgggaaacaataatctctacgtgaagacgagaaactggggagatggtg 480  
QY 481 AGCCCAACAACAAGAAACAAGAGAGACTGGGTGAGATCTATATCAAGAGAAACAAG 540  
Db 481 agcccaacaacaagaaacaagagagactgggtgagatctatatacaagagaacaag 540  
QY 541 ATGCAGCAATGAGAGCATGACGCTGCGCACAAACTAAAGCAGCCCTCTGTTACAG 600  
Db 541 atgcagcaatgagagcatgacgctgCGCACAAACTAAAGCAGCCCTCTGTTACAG 600  
QY 601 CTTCCTGGCAGCCCTGCTATGATGAGTGGCATGGCATGGAATGTTAGAAATCATATATC 660  
Db 601 ctctctggcagccctgctatgATGAGTGGCATGGCATGGAATGTTAGAAATCATATATC 660  
QY 661 ACACCTGCAACTGTGATGTGGGTACTATGGGCCCCAGCTGATGTTGATGATGATG 720  
Db 661 acacctgcaactgtgATGTGGGTACTATGGGCCCCAGCTGATGTTGATGATGATG 720  
QY 721 AGCCTTTGAGAGGCCGACAGCTGGGTACCATGAGACTGTACTACCCCTTTGAAACTTCA 780  
Db 721 agcctttgagagggccgacagctgggtacCATGAGACTGTACTACCCCTTTgaaacttca 780

QY 761 GCCTTCAGCTCAGAGTGTGCGCTTACGCTGCTGTAAGGAACAACCTTAACCTGGAGTTGAG 840  
 DB 761 gcttcagctcagagtggtcgttcagctgctcgtgaaggaacaaacttaactgagatcgag 840  
 QY 841 AACCACCTGTGACCATTTTGGAAACGTGTCATCTCCAGAACCAACCTGTCAAGTGATTC 900  
 DB 841 aaacacactgtgacacattggaacactggtacatccacgaacaaacbtgcaagtgtatcc 900  
 QY 901 AGTGTGAGCTCTATCAGACCAAGATTTGGGATCATGAACTGTGACCTGCCCTGGCCA 960  
 DB 901 agtgtgagctctatcagaccagacatctgggagatcagacgtgagccatcccccggcca 960  
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 QY 1021 AGACAAAACCACTTTTGTGATCATCTGCAATCTGCTCAATCTCAATCTGCAAT 1080  
 DB 1021 agaagaaaacacatctgtgatacatctggaatctggtcaaatccatagtcacaatgltcaa 1080  
 QY 1081 AATTGACAAAAGTTTCTCAATGATTAAGAGGATTAATTAACCCCTCTCATCTCCAG 1140  
 DB 1081 aattgacaaaagttctcaatgattaaaggaggtgattataaacccctctcatccag 1140  
 QY 1141 TGGCAGTCACTGCTACTGCAATCTCTGGGTTGGCATTTATCATTTTGGCTGCAAGAGAT 1200  
 DB 1141 tggcagtcactgctactgcaatctctgggttggcattttattcatTTTGGCTGCAAGAGAT 1200  
 QY 1201 TAAAAAAGCAGAAATTCAGAGAGAGTANGAATGACCCATATTAATTCGCCCTTGGTG 1260  
 DB 1201 taaaaaagcagaataccaaagagaatlatgaatgccatataatcgcccttgg 1260  
 QY 1261 AAGAAATTTCTTGGATTAATAATCATGATCCTTTAATCTTCCATGAAGATCTT 1320  
 DB 1261 aaagaatatcttggataactaaatacaatgagatcccttaaacctctccatgaaacgtt 1320  
 QY 1321 TTGTGTGCTGGCAGCTCTTACGTCATCAACATGAGTGTGTCCTTCAGTGCATCTGGAG 1380  
 DB 1321 ttgtgtgctggcagctcttaccgtcacaacatgagtggtgtccttcagtgcatctggagag 1380  
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 DB 1381 attttaccgcagcaacagttcctctcagcttccatctcgccctcatattatccctcaacc 1440  
 QY 1441 CCCACCCACAGGCTTATATACAGCTCAGCTTTTGTCTTTCTGAGGAAACAATAA 1500  
 DB 1441 cccacccacaggtgttatacagctcagcttctgtccttctcgaaggagaaacaataaa 1500  
 QY 1501 GACCATTAAGGGAAGATTCATGTGAATATTAAGATGGCTGACTTGTCTTTCTTGAC 1560  
 DB 1501 gacctaaagggaagatctcatgctggaatataaaga tggcgtgacttctccttcttgag 1560  
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 DB 1561 tctgtgttctcagttccaattcagtgctgtactgtgtgacagacacttctaaatgaaagtcg 1620  
 QY 1621 AATTTGTATCATATGTGAATATGACATCAGTTTCTTTCAGATCAAAATTTTACGTCGTC 1680  
 DB 1621 aaattgtatacatgtaataatgtaactcagtttctctgcagataaaatltcacgtctgc 1680  
 QY 1681 TTTCTGTATACGTGTGAGAGTACACTCTTATAGAAAGTTCAAAAAGTCTACGGCTCTCTTTTC 1740  
 DB 1681 ttctgtataacgtgtgagagtaacatcttataagaagttcaaaaagttcagacccctctcttc 1740  
 QY 1741 TTTTCTAATCTCAGTGAAGTAAATGGGCTCTGCTCAAGTTGAAGAGTCTTATTTTCACATG 1800  
 DB 1741 ttcttaactccagtgaaatgaatggggtctcgtcgaagtgaagaaggtctctatttgacatg 1800  
 QY 1801 TAGCCTCGCGTGTGTGAATTTGACCATCTTATTTAATGAGCTTGAAGGCTCTCCACCTT 1860  
 DB 1801 tagcctcgcgctgtgtgaatttgacacatcctaatttaactggtctcagagcctccacactt 1860

QY 1861 CTTTCAGCCACCTCTCTTTTTCAGTTGGCTTGACCTTCACACCTTAGCAATTCATGAGTGCCA 1920  
 DB 1861 ctctcagccacctctcttcttctcagtttgactgacttccacacctagacatgtcatgagtgcca 1920  
 QY 1921 AGCAAAAGAGAGAGAGAGAAATAGCTTCGCGGCTTTTATGTTTGGGGCTTTGCTGT 1980  
 DB 1921 agcaaaagagagagagaaatagccttcgcggttcttcttcttcttcttcttcttcttct 1980  
 QY 1981 TTTCTTTTATGAGACCCATCTCTATTTCTTATAGTCAATGTTTCTTTTATCAGATATTA 2040  
 DB 1981 ttctcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 2040  
 QY 2041 TTAGTAAGAAACATCACTGAATGCTAGCTGCAAGTGAATCATCTGTTGATGTCAATG 2100  
 DB 2041 ttagtaagaacacatcaccgaatctgactgcaagtgacatcctcttcttcttcttcttctt 2100  
 QY 2101 AAGAGTTAAACAGTGGAGAAATTCCTTGTGATTCACATGAATGCTCTCTTTCCCTG 2160  
 DB 2101 aagagttaaacagtgaggaaatctccttgatctcaacatgaaatgctcctcttccctg 2160  
 QY 2161 CCCCCAGAACCTTTATCCACTACCTAGATTCATATCTTTAATTTCAATCTCAGGC 2220  
 DB 2161 cccccagaaacttcttaccacttaccatctagatctctacatattcttcaattctcagc 2220  
 QY 2221 CTCCCTCAACCCACGCGGCGCCGACGACACATGGAATTC 2259  
 DB 2221 ctccctcaacccacgagggcgcgacacacatcgaaatc 2259

RESULT 9  
 Q23623  
 ID Q23623 standard; DNA: 2260 BP.  
 XX  
 AC Q23623:  
 XX  
 DT 01-SEP-1992 (first entry)  
 XX  
 DE Human lymphocyte homing receptor gene.  
 XX  
 KW HulHR; LHR; binding; endothelium; immunogens; graft; organ; ss;  
 KW rejection; inflammation; rheumatoid arthritis; lymphoma metastasis.  
 OS Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 129..1248  
 FT /\*tag= a  
 PN US5098833-A.  
 XX  
 XX 24-MAR-1992.  
 PD  
 XX 23-FEB-1989; 89US-0315015.  
 PF  
 XX 23-FEB-1989; 89US-0315015.  
 PR  
 XX (REGC ) UNIV OF CALIFORNIA.  
 PA  
 XX Lasky LA, Rosen SD, Stachel SE, Singer MS, Yednock TA;  
 PI WPI; 1992-123385/15.  
 DR P-PSDB; R22802.  
 DR  
 PT New DNA encoding at least one domain of lymphocyte homing  
 PT receptor - useful for treating graft rejection, inflammation,  
 PT etc.  
 PS Claim 3; Fig 1; 32pp: English.  
 XX  
 CC The DNA sequence was obt'd. by screening an oligo dt primed lambda  
 CC g10 cDNA library derived from human peripheral blood lymphocyte  
 CC mRNA obt'd. from primary cells, with a 2.2 kb EcoRI insert of the  
 CC murine Mel 14 antigen cDNA clone. 12 positive plaques were isolated



CC and those with the largest EcoRI insert were sequenced. The 2.2 kb  
CC clone encodes an open reading frame of 372 amino acids. The human  
CC LHR is 83 percent homologous with the murine LHR sequence and  
CC contains regions encoding a carbohydrate binding domain, an EGF-like  
CC domain, a complement binding domain and a transmembrane domain.  
CC Cells transformed by the hLHR DNA are used to produce LHR (which  
CC mediates binding of lymphocytes to the endothelium of lymphoid  
CC tissue). LHR or its variants are useful as reagents for assaying  
CC LHR or anti-LHR antibodies, to purify the antibodies, as immunogens,  
CC and therapeutically to compete with normal binding of lymphocytes  
CC (to prevent graft/organ rejection; to treat inflammation (such as  
CC rheumatoid arthritis or other autoimmune diseases); for control of  
CC lymphocyte metastasis, and to treat conditions associated with  
CC accumulation of lymphocytes). Derivs. and variants of LHR may be  
CC produced having modified properties, e.g. increased activity, longer  
CC plasma half-life, reduced side effects and better aq. solubility.  
CC See also Q23624 and Q23464.

XX Sequence 2260 BP; 636 A; 518 C; 487 G; 619 T; 0 other;

Query Match 99.2%; Score 2241.6; DB 13; Length 2260;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2244; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAATTCAGTGTGCTGCTTCTCACTGACAGACACACTCCCTTGGCAGAGACT 60  
Db 1 gaattcagtgctgtcctcctcctcctcctcctcctcctcctcctcctcctcct 60  
QY 61 GAGACCTTGTGCTAAGTCAGAGAGGCTCATGSGGTGAGAGAACTAGAGAACCA 120  
Db 61 gagaccttgctgaagtcagagagggctcagagctcagagaaactccttgggaag 120  
QY 121 GCAGAGCCATGATATTTCCATGGAATGTCAGAGCACCAGGAGCTTATGACATCT 180  
Db 121 gcaagccatgatattccatggaatgtcagagaccagagagcttattggaactct 180  
QY 181 TCAAGTTGGGGGGTGAGCAATGCTCTGTGATTTCTTGACATATGAGAACTACT 240  
Db 181 tcaagttgggggtgagcaatgctctgtgatttcttgacatattgaaactact 240  
QY 241 GCTGAGCTTACCATATTTCTGMAAAACCATGAACTGGCAAGGCTTGAAGATTCC 300  
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QY 361 AGACTGCGCCTTCAGTCTTCTACTACTGATAGGAATCCGAAAGTAGAGGAATAT 420  
Db 361 agactcgcccttcagtcttctactactgataagaaatccggaatagagaatata 420  
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Db 421 ggaagctgggtgggaaccaaacaatctctcactgaagaagcagaactggggaatg 480  
QY 481 AGCCCAACACAGACAGAACAGAGAGACTGCTGGAGATCTATATCAAGAGAAACAAG 540  
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Db 541 atgagagcaatgagagatgagcgctgcacaaactaaaggacgcccctgttacaacag 600  
QY 601 CTTCTTGCCAGCCCTGTGTCATGCAAGTGGCCATGAGAAATGTGTAAGAAATCATCAATATC 660  
Db 601 ctctctgcccagccctgtgtcatgcaagtggccatgagaaatgtgtagaatacataa 660  
QY 661 ACACCTCAACTGTGATGTGGGTACTATGAGGCCCAAGTCTACGCTTGATTCAGTGTG 720  
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QY 721 AGCCTTGGAGGCCCCAGAGCGTGGGTACCATGAGACTGTAACCCCTTTGGAAACTTCA 780  
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Db 1441 cccagccacaggtgttatacagctcagcttcttcttcctcgtgaggaacaataa 1500  
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QY 1681 TTCTGTATACCTGTGGAGGTACACTCTTATAGAAAGTTCAAAAAGCTTACGCTTCCTTC 1740  
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Db 1861 cttagcaccactctctcttcttagtgcgtgactccacacacatcctcatgagtgccca 1920
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QY 2101 AAGAGTTTAAACAGGTGAGAGAAATTCCTTGAATTCACAAATGAATGCTCTCCCTTCCCTG 2160
Db 2101 aagagctaaacaggttgagaaatctccttgatctacaatgaaatgctctctctccctg 2160
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Db 2161 cccccagacttctatccactacatagatctacatatctcttaattcatcacaagc 2220
QY 2221 CTCCCTCAACCCGACGGGGCGCCGACGA 2248
Db 2221 ctccctcaaccacagggcgccgacga 2248
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RESULT 10
Q24987
ID Q24987 standard; DNM: 2262 BP.
XX
AC Q24987;
XX
DT 22-NOV-1992 (first entry)
XX
DE Sequence encoding human lymphocyte cell surface glycoprotein
DE (HLHR).
XX
KM Lymphocyte cell surface glycoprotein; ligand binding protein; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 129..185
FT FT /*tag= a
FT FT 186..242
FT FT /*tag= b
FT FT malt-peptide 143..1247
FT FT /*tag= c
XX
PN US5116964-A.
XX
PD 26-MAY-1992.
XX
PF 22-NOV-1989; 89US-0440625.
XX
PR 23-FEB-1989; 89US-0315015.
PR 22-NOV-1989; 89US-0440625.
XX
PA (GENTECH ) GENENTECH INC.
XX
PI Capon DJ, Lasky LA;
XX
DR WPI: 1992-199589/24.
DR P-PSDB; R24026.
XX
PT Nucleic acid encoding polypeptide fusions - comprising ligand
PT binding partner protein and immunoglobulin chain, for use in
```

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PT diagnosis and therapy
XX
PS Disclosure: Fig 1-1 - 1-3: 43pp; English.
XX
CC LHR mediates the binding of lymphocytes to the endothelium of
CC lymphoid tissue. Full length cDNA clones and DNA encoding the human
CC and the murine LHR (HLHR and MLHR, respectively) have been
CC identified and isolated (see Q24987 and Q24988). LHR is a
CC glycoprotein which contains the following protein domains: a signal
CC sequence, a carbohydrate binding domain, and epidermal growth
CC factor-like (egl) domain, at least one and preferably two complement
CC binding domain repeat, a transmembrane binding domain (TMD), and a
CC charged intracellular or cytoplasmic domain. LHR is used as the
CC ligand-binding partner in fusion polypeptides with an immunoglobulin,
CC for use in diagnosis and therapy.
XX
SQ Sequence 2262 BP; 635 A; 518 C; 488 G; 621 T; 0 other:
Query Match 99.2%; Score 2241.2; DB 13; Length 2262;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2256; Conservative 0; Mismatches 3; Indels 3; Gaps 1;
QY 1 GAATTCAGGTGTGCTGGCTTCCTCAGCTGCAGACAGACAGACTCCCTTTGGCAAGACT 60
Db 1 gaattcaggtgtgctgcttcctcagctgcagacagacagactcctttggaagacct 60
QY 61 GAGACCCCTTGCTGCTAAGTCAGAGAGGCTCATATGGCTGCAGAGAACTGAGAGACCA 120
Db 61 gagacccttgctgcttagtcaagaagctcatatgctgcaagaactagagagaccaa 120
QY 61 GCAAGCCATGATATTTCCATGAGAAATGTCAGAGACCCAGAGGAGATATGGAACATCT 180
Db 121 gcaagccatgatatcttcacatgagaaatgtaacagagaccagagagactatagaaacatc 180
QY 181 TCAAGTTGSGGGTGGACAATGCTCTGTGTGATTTCTGTGACATCATGGAACCTACT 240
Db 181 tcaagttgsggggtggacaatgctctgtgtgatctgtgacatcatggaacctact 240
QY 241 GCTGACTTACCATTTCTGAAAACCCATGAACTGGCAAAAGGCTGTGAAGATTCTGCC 300
Db 241 gctgacttacatcttctgaaaaccatgaaactggaagggctgaaagatcttgc 300
QY 301 GAGACAATTACACAGATTAGTTGGCATACAAACAGCGGAATTTAGTATCTGAGCA 360
Db 301 gacacaattacacagatttagttggcatacaaacagcggaatttagatctcggaga 360
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Db 361 agacttcgcccttcagtgttctactactgataagatccggagatagagaaatc 420
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Db 421 ggaagtgggtgggaaccaaattctctactgaagaaagcagaagactgggagatg 480
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Db 481 agcccaacacagagagaaagagagagctgctgagatcatatcaagaaacaaag 540
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Db 541 atgcaggaatggaacgatgacgctgccacaacatttaaggacccctctgttacaag 600
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Db 601 cttcttgccagccctgatgatgagtgcccatgagaaatgttgaaatcattaatac 660
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Db 661 acacctgcaactgatgtgggtactatgggcccatctgagttgttgattagtg 720
QY 721 AGCCTTTGGAGCCCAAGAGCTGGTACCATGAGACTGTACTACCCCTTTGGAACATTTCA 780
Db 721 agcctttggagcccaagagctgggtaccatgagactgtactacccctttggaacatttca
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Db 721 agccttggaggccccagagctgggtaacatggaactgtaactcaccaccttggaaacttca 780
Qy 781 GCTTCAGCTCAGAGTGTGCTCTTCAGCTGCTGTGAAGAAACAATTAATGCGGATTGAAG 840
Db 781 gcttcagctcagtgtagcttcacgctcgcttcgaaggaaacaacttaactgagggttgaag 840
Qy 841 AAACCCACTGTGAGCACTTTGGAAACGTGTCATCTCCAGAACCAACCTGTCAAGTGAATTC 900
Db 841 aaaccacctgtgagaccatttggaaactgtaactcctcagaaaccaactgtcgaagtgaatc 900
Qy 901 AGTGTGAGCCCTATCAGCAACCCAGATTTGGGGATGATGAAGTGTGAGCATCCCTGGCCA 960
Db 901 agtgtgagccctatacagaccagatttggggatcagtaactgtaagccatccctcgcca 960
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Qy 1141 TGGCAGTCATGTTACTGCAATTCCTGTGGGTTGGCATTTATCATTTTGGCTGGCAAGAGAT 1200
Db 1141 tggcagtcactggttactgactctctcggttggcatttaccatttggctggcaaggaggt 1200
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Qy 1261 AAGAAAA---TTCCTGGAATCTAAAAATCATGAGATCCTTAAATCCTTCATGAAGAC 1317
Db 1261 aagaanaattctcttggaaactaataaatacatgagatcctttaaactccttcaagaac 1320
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Db 1321 gtttgtgtggtggaacccctcaagtcacaaatgaagtgttcttcaagtgacatctggg 1380
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Qy 1438 ACCCCAGCCGACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGAGAAACAA 1497
Db 1441 accccagcccgacaggtgttatacagctcagcttcttcttcttctgagagaacaa 1500
Qy 1498 TAAGACATTAAGGAAAGATTCATGTGGATTAAGATGGGTGACTTCTCTTTCTT 1557
Db 1501 taagacataagggaaagatcatctgtaataaataaagaatgagcttgcacttcttct 1560
Qy 1558 GACTCTTGTTCAGTTTCAATTCAGTGTCTGACGTGATGAGACACTTTTAATGAAG 1617
Db 1561 gactcttgttctcagtttcaatcagtgctgtacttgaagcagacacttctaagaag 1620
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Qy 1738 TTCTTTTCTAATCCAGTGAAGTAATGGGGTCTGCTCAAGTGTGAAGAGTCTATTGCA 1797
Db 1741 ttcttcttaactccagtgaaatgaggttcctgctcaagtgtgaagagttccatttga 1800
Qy 1798 CTGTAGCCTGCGCGTGTGTAATGAGCAATCTGATTTAACTGGCTTCAGGCTCCGCCAC 1857
Db 1801 ctgtagcctgcgcgtctgtaattggacacatctatttaactgtctcaggtctcccca 1860

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Qy 1858 CTTCCTCAGCCACCTCTCTTTTTCAGTTGGCTGACTGATCCACACATGATCATGAGTG 1917
Db 1861 ctctctcagccacactctcttcttctcagtttggtgacttccacacactcagatcatgagtg 1920
Qy 1918 CCAAGCAAAAGAGAGAGAGAGAAATAGCTGCGCGGTTTTTTTAACTTTGGGGTTTTGCG 1977
Db 1921 ccaagcaaaaggagagagaaatagcctgcgcggttctttagtttgggttttgc 1980
Qy 1978 TGTTCCTTTTATGAGACCCATTCCTATTTCCTTATAGCATAGTTCTTTATACAGATA 2037
Db 1981 tgttcctttatgagaccacttccattcttctttagtcaatgcttcttatacagata 2040
Qy 2038 TTATTATGTAAGAAACATCAGTAATGCTAGCTGCAAGTGACATTCCTTTGATGATA 2097
Db 2041 ttattatgaagaaacaacactcgaatgctagctgcgaagtgacatctctttagatcata 2100
Qy 2098 TSGAAGAGTTAAACAGGTGAGAAATTCCTTGATTTACAAATGAAATGCTCTCCTTGCC 2157
Db 2101 tggaaagatttaaaacaagctggaataatccttgatctacaatgaaatgctctcctccc 2160
Qy 2158 CTGCCCCGAGAACTTTTATCCACTTACCTAGATTCTACATATTCCTTAAATTCATCTCA 2217
Db 2161 ctgccccagaaacttataccacttacctagattctacatattcttaaatcattca 2220
Qy 2218 GGGCTCCCTCAACCCGAGGCGCGCCAGCACACTGGAATTC 2259
Db 2221 gggctccctcaaccgcaagggcgcgagcacactggaattc 2262

RESULT 11
T14723
ID T14723 standard: cDNA: 2350 BP.
XX AC
XX T14723:
DT 31-OCN-1996 (first entry)
XX
DE Human Leu8 antigen cDNA (major transcript).
XX
KW Cell surface antigen; cloning; immunoselection; immunotherapy;
therapy; diagnosis; vector; COS; Leu9; T-lymphocyte; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 50..1207
FT FT /*tag= a
FT misc_feature 1079..1514 /*tag= b
FT FT /note= "bases 1079-1514 are deleted in the
XX shorter cDNA clone"
PN US5506126-A.
PD 09-APR-1996.
XX
PF 25-FEB-1988; 88US-0160416.
XX
PR 01-DEC-1992; 92US-0983647.
PR 25-FEB-1988; 88US-0160416.
PR 13-JUL-1989; 89US-0379076.
PR 13-JUL-1990; 90US-0553759.
PR 18-OCT-1993; 93US-0139273.
XX
PA (GEMO ) GEN HOSPITAL CORP.
PI Aruffo A, Seed B;
XX
DR WPI: 1996-200279/20.
DR P-PSDB: R91442.
XX
XX Cloning of cDNA encoding cell surface antigen - useful for isolation
PT

```







SO Sequence 2350 BP; 679 A; 521 C; 489 G; 661 T; 0 other;

Query Match 94.1%; Score 2126.2; DB 19; Length 2350;  
Best Local Similarity 99.2%; Pred. No 0;  
Matches 2178; Conservative 0; Mismatches 13; Indels 4; Gaps 4;

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OY 44 CCCCTTGGCAAGACCTCGAGACCCCTTGTGTAAGTCAAGAGCGCTCAATGGCGTCGACAG 103
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Db 4 ccttgggcaagagacctgagaccttgctgtaagtcgaaggcctcaatggtcgccgaaag 63

OY 104 AACTAGAGAAAGGACCAAGCAAAAGCATGATTTCCATGGAATGTCAGACACCCAGAG 163
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Db 64 aactaagaagaagcaagcaagcaagcaltgatalctccatggaatgltcaagagcaccagag 123

OY 164 GGACTTATGGAACATCTTCAAGTTGTGGGGGTGGACAACTCTGTTGTGATTTCCGTGGC 223
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OY 224 ACATCATGGAACCTACCTGCTGAGCTTACCATTTATCTGAAAAACCATGAATGGCAAG 283
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Db 184 acatcatggaacccgactgctggaacttaacctatctctgaaaaaccatgaaactgcaag 243

OY 284 GGCTAGAGAACTTGGCCGAGACAAATTACAGATTTAGTTGCCATACAAACAGCGCA 343
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 ggcctagaagaattctgcgcgagaacattacaagaattagctgcatacaaaagaagcgga 303

OY 344 AATTGATATCTGAGAAGACTCTGCCCTTCACTGCTTCTTACTACTGATAGAAATCGG 403
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Db 304 aattgatatctgagaagaactctgaccttcgaagtgttcttactactgataagaaatccg 363

OY 404 GAAGATAGAGAGATATGACGCGGTGGGGAACCAACAAATCTCTCACTGAAGACAGA 463
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OY 464 GAACCTGGAGATGCTGACCCCAACAACAAGAAGAAAGAGAGAGCTGGCTGGGAATCTA 523
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OY 524 TATCAAGAGAAACAAAGATGACAGCAATGGAACGATGACGCTCCCAAACTAAAGGC 583
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Db 484 tatcaagaaacaagaatgacgacaatggaacgtgacgctcgccaacaactaaagac 543

OY 584 ACCCCTCTCTACAGAGCTTCTGGACGCCCTGGTCATGACAGTGGCCATGGAAGATGTGT 643
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OY 644 AGAAATCATCAATTAATCACACCTGCAACTGTGATGTGGGTACTATGAGGCCCCAGTGA 703
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OY 704 GCTTGATTCAGTGTGAGCTTTGGAGAGCCCGAGAGCTGGGTACCATGACCTTACTCA 763
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OY 764 CCCCTTTGAAACTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAGCTTCAG 823
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OY 824 CTTAACCTGGGATTGAGAAGAACCACTGTGAGACATTTGGAACATGTCATCTCCAGAAC 883
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Db 784 cttaactggtatgtgaagaacacacctgtgagccatttggaaactggtcaltctccagacc 843

OY 884 AACTGTCAATGATTCAGTGTGAGCTTCATACAGCAACGATTTGGGGATCATGAATCG 943
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OY 944 TAGCCATCCCTGGCCAGCTTTCAGCTTACCTTCGATGACCTTCATCTGCTCAGAGG 1003
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OY 1004 AACTGATTAATTGGGAAGAAACCAATTTGTGAATCATCTGGAATCTGTCAATCC 1063
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OY 1184 TTGGCTGGCAAGGATTAATAAAGCAAGAAATTCAGAGAAAGTATGATGACCATTA 1243
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OY 1304 TCCCTTCATGAAGGTTTGTGTGTGGTGGACCTCTTACGTCAACATGAAGTGTG-TTCC 1362
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OY 1722 AAGTCTACGCTCTCTTTCTTCTAACTCAGTGAAGTAATGGGGTCTGCTCAAGTGA 1781
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OY 1902 TTGACATCTGATGAGTGCAAGCAAAAGAGAGAGAGAGAAATAGCCTGGCGGTTTTTT 1961
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OY 2082 TCTCTTTGATGTCATATGGAAGAGTAAACAGGTGGAAGAAATTCCTTGATTACAAATGA 2141
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Db 2043 tctcttgatgcatataggaaggttaaacaggttggaagaattcttctgtatcaaatga 2102
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QY	2142	AAACCTCCTCCTTTCCCTCGGCCCAACAATTTTATTCG - ACCTACCTACCAATTTCTACATATTT	2200
Db	2103	aaagctctcccttcccccgcgcacacaccttatactcagctactcagatctctacataatt	2162
QY	2201	CTTTTAAAATTTTCATCTCAGGCGCTCCCTCAACGCCAC	2235
Db	2163	ctttaaatttcacatcctcagcgtctccctcacaaccac	2197





QY	44	CCCTTTGGCAAGACACTGAGACCTTTGTGCTAAGTCAAAGGCTCAATGGGCTGCAGAAAG	103
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QY	154	GGACATTTATGGAACATCTTTCAAGATTGTGGGGGTGGCAATCATCTGTGTTGTGATTTTCCGTGC	223
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QY	224	ACATATATGGAACCTTACTGCTGGACTTTACCATTTATCTTGAAAAACCATGACTGGCAAG	283
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QY	284	GGCTTGAGAGATTTTCGCGCAGACATTTACACAGATTTTGTGGCATTCGATTCGCAAAACGAGCGCA	343
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QY	344	AATTTGAGTATCTGGAGAGAAGACTTCTGCCCTTTCACTGCTTTTACTACTGGATAGAGATTCGG	403
Db	307	aattgagatctcgtgaagagactctgcgctcttcagtcgctctctactactcgtatagaaatcgc	366
QY	404	CAGATATGAGGAGAAATATGAGACGTGGGTGGAGACCAACAATCTCTCTACGTAAGAGACAGA	463
Db	367	gaagaatagagaaatatagaaatgtgtgtgggaaccaaacaatctctcaactgaagaagcaga	426
QY	464	GAACGTGGGACATATGTGAGGCCCAACAACAAGAAACAAGAGAGACTGGGTGGAGATCTTA	523
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QY	524	TATCAAGGAAACAACAAGATGAGAGCAATGGAAGATGAGAGCTTGCCACAACTTAAGAGC	583
Db	487	tatcaagagaaacaagaatgcaagcacaatggaagatgagacgctgtccacaacaactaaagac	546
QY	584	AGCCCTCTGTTCACACAGCTTCTTGCCAGCCCTGGTCTATGCAATGGCCATGAGAAATGTGT	643
Db	547	agccctctgttacaacagcttcttcgcagccctgtgtcatgtgacgtgagacatgagaatgtgt	606
QY	644	AGAAATCATCATTAATATCAACACCTTCACACTGTGATGTGGGTACTATATGGGCCCCAGTGTGA	703
Db	607	agaaatctcaataatctaacactgcagacatgtgagatgtgaggttactatcagggcccaagtcca	666
QY	704	GCTTTCTGATTTAGATGTGAGCCCTTTGGAGGCCCCAGAGACTGGGTATACCATGAGACTGTCTCA	763
Db	667	gttctgtgactcaagtgtgagagccttctggagggcccaagagctcgtgtatccaatgagactgtactca	726
QY	764	CCCCCTTTGGAAACTTTCAGCTTCAGCTTCACAGTGTGCTTCAGCTGTCTGAAAGGAACAA	823
Db	727	cccttctggaaacttcaacttcaactcaacacagttgtccttcagtgctctcgaaggaacaaa	786
QY	824	CTTAACTGCGGATTTAACAACAACCACTGTGTGACCACTTTGGAAACTGGTCAATCTCCAGAAC	883
Db	787	cttcaactctggagatctgaagaacaacacctctgaaacatcttggaactctgtctctccagaacc	846
QY	884	AACGCTTCACACTGATTTAGTGTGAGTGGCCCTTATCAGACACAGATTTTGGGGATCATGTGAATG	943
Db	847	aaactgtcagaagtgtatcaagtgtgagggccttcataagcaaccagaatcttggagatcaatgaaacg	906
QY	944	TAGGCATCCCTTGCGCAGCTTTCAGCTTTACCTCTGCATGTACTTTCATCTTGCTGCAGAAAG	1001
Db	907	tagcacaatccctctgcagagcttcagctttactcctctgataacttcaatctgtctcagaag	966
QY	1004	AACGTAGCTTAATTTGGGAAGAAGAAACCAATTTGTGAATCATCTGGAATCTGGTCAATTC	1061
Db	967	aactgtagatctaatcttggaagaagaanaaccatctctgaaatcatctcgaatctcgttcaaatcc	1020
QY	1064	TATGTCATTAATGTCAAAAAAATTTGGCAAAAGCTTTCTCATATGATTAACGAGAGGTGATTTATA	1122
Db	1027	tagttccaatactgccaataaatttggcacaagaatcttcccaatgataaaggaggtgagattataa	1086
QY	1124	CCCCCTTTCAATTCACAGTGGCAGTCAATGAGTTACTGCAATTTCTCGGGTCTGGCAATTTATCAT	1183

[illegible]

Db 2160 ttaaattcattcagggcctccctcaaccccaac 2193

Search completed: January 13, 2001, 00:37:12  
Job time: 16618 sec

\* \* \*

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 12, 2001, 16:24:14 : Search time 79.76 seconds  
(without alignments)  
4564.457 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259  
Sequence: 1 GAATTCGACTGTGCTGCTT.....CCGCACGACACTGGAATTC 2259

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 280836 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_MA: \*  
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4: /cgn2\_6/ptodata/2/lna/PCrUS-COMB.seq: \*  
5: /cgn2\_6/ptodata/2/lna/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	2259	100.0	2259	2 US-08-513-278-1	Sequence 1, Appli
2	2087.6	92.4	2330	1 US-08-481-803-1	Sequence 1, Appli
3	2087.6	92.4	2330	1 US-08-215-366A-1	Sequence 1, Appli
4	2087.6	92.4	2330	1 US-08-340-539A-1	Sequence 1, Appli
5	2087.6	92.4	2330	2 US-08-461-592B-1	Sequence 1, Appli
6	1469.2	65.0	1829	5 5514582-1	Patent No. 5514582
7	922.2	40.8	1696	2 US-08-340-539A-11	Sequence 11, Appli
8	922.2	40.8	1696	2 US-08-461-592B-11	Sequence 11, Appli
9	856.8	37.9	2214	5 5514582-3	Patent No. 5514582
10	856.8	37.9	2214	5 5514582-3	Patent No. 5514582
11	385.2	17.1	531	2 US-08-461-592B-5	Sequence 5, Appli
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13	310	13.7	1833	3 US-09-209-668-18	Sequence 18, Appli
14	310	13.7	3834	3 US-08-365-470-1	Sequence 1, Appli
15	310	13.7	3834	1 US-08-340-539A-8	Sequence 8, Appli
16	310	13.7	3834	1 US-08-340-539A-7	Sequence 7, Appli
17	310	13.7	3834	1 US-08-340-539A-9	Sequence 9, Appli
18	294.8	13.1	3144	4 PCT-US91-05059-1	Sequence 1, Appli
19	294.8	13.1	3144	4 PCT-US91-05059-1	Sequence 1, Appli
20	240.2	10.6	2989	5 5378464-1	Patent No. 5378464
21	223.4	9.9	1592	2 US-08-252-493C-1	Sequence 1, Appli
22	223.4	9.9	1592	3 US-09-276-197-1	Sequence 1, Appli
23	189.4	8.4	451	1 US-08-340-539A-8	Sequence 8, Appli
24	189.4	8.4	451	1 US-08-461-592B-8	Sequence 8, Appli
25	183.8	8.1	712	2 US-08-461-592B-7	Sequence 7, Appli
26	183.8	8.1	712	2 US-08-340-539A-9	Sequence 9, Appli
27	131.2	5.8	544	2 US-08-461-592B-9	Sequence 9, Appli
28	131.2	5.8	544	2 US-08-461-592B-9	Sequence 9, Appli

#### ALIGNMENTS

29	107.2	4.7	832	1 US-08-340-539A-6	Sequence 6, Appli
30	107.2	4.7	832	2 US-08-461-592B-6	Sequence 6, Appli
31	96.4	4.3	1192	1 US-08-340-539A-3	Sequence 3, Appli
32	96.4	4.3	1192	2 US-08-461-592B-3	Sequence 3, Appli
33	84.2	3.7	363	1 US-08-340-539A-4	Sequence 4, Appli
34	84.2	3.7	363	2 US-08-461-592B-4	Sequence 4, Appli
35	57.6	2.5	7218	1 US-08-232-463-14	Sequence 14, Appli
36	47.4	2.1	7218	1 US-08-232-463-14	Sequence 14, Appli
37	37	1.6	1430	1 US-08-798-744-25	Sequence 25, Appli
38	37	1.6	1430	2 US-07-867-106-2	Sequence 2, Appli
39	37	1.6	5852	1 US-08-465-794-4	Sequence 4, Appli
40	35.8	1.6	1179	2 US-09-049-813-4	Sequence 4, Appli
41	35.8	1.5	1700	2 US-08-897-340-4	Sequence 4, Appli
42	33.6	1.5	1700	3 US-09-252-329-4	Sequence 4, Appli
43	33.6	1.5	3441	2 US-08-525-864A-1	Sequence 1, Appli
44	33	1.5	1560	1 US-07-668-171-1	Sequence 1, Appli
45	32.8	1.5	1560	1 US-07-668-171-1	Sequence 1, Appli

RESULT 1  
US-08-513-278-1  
: Sequence 1, Application US/08513278  
: Patent No. 5840844

#### GENERAL INFORMATION:

APPLICANT: LASKY, LAURENCE A.  
APPLICANT: STACHELL, SCOTT E.

APPLICANT: ROSEN, STEVEN D.

APPLICANT: SINGER, MARK S.

APPLICANT: YEDNOK, TED A.

TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 Inch, 360 KB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/513.278

FILING DATE: 10-AUG-1995

CLASSIFICATION: 5530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/059027

FILING DATE: 06-MAY-1993

APPLICATION NUMBER: 07/786149

FILING DATE: 31-OCT-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/315015

FILING DATE: 23-FEB-1989

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 33,055

REFERENCE/DOCKET NUMBER: 565D1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-3216

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2259 bases

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-513-278-1

Query Match	100.0%;	Score 2259;	DB 2;	Length 2259;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2259;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	1	GATTCACAGTGTGCTGGCTTCCTCACCTGTGACAGACAGCACTCCCTTTGGCAAGGACCT	60
Db	1	GAATTCACAGTGTGCTGGCTTCCTCACCTGTGACAGACAGCACTCCCTTTGGCAAGGACCT	60
OY	61	GAGACCCCTTGTGTAAGTCAAGAGGCTCAATGGGTGCAGAAAGACTGTGACAAGACC	120
Db	61	GAGACCCCTTGTGTAAGTCAAGAGGCTCAATGGGTGCAGAAAGACTGTGACAAGACC	120
OY	121	GCAAAGCCATGATATTTTCCATGGAAATGTCAAGCAGCACCAGAGGACTTATGAAACATCT	180
Db	121	GCAAAGCCATGATATTTTCCATGGAAATGTCAAGCAGCACCAGAGGACTTATGAAACATCT	180
OY	181	TCAAGTGTGGGGGGTGGACATATGCTGTGTGATTTCTGTGGACATATGTGAACCTACT	240
Db	181	TCAAGTGTGGGGGGTGGACATATGCTGTGTGATTTCTGTGGACATATGTGAACCTACT	240
OY	241	GTGGAGCTTACCAATTTATTTGTGAAAAACCATGATACCTGCCAAAGGCTTGAAGATTGCGC	300
Db	241	GTGGAGCTTACCAATTTATTTGTGAAAAACCATGATACCTGCCAAAGGCTTGAAGATTGCGC	300
OY	301	GAGACATTTACACAGATTTAGTTGGCATACAAACAAAGCGGAATTTAGATTTGTGAGA	360
Db	301	GAGACATTTACACAGATTTAGTTGGCATACAAACAAAGCGGAATTTAGATTTGTGAGA	360
OY	361	AGACTGTGGCCCTTCAAGTGGTCTTCTACTACTGTGATGAGATTCGGAAATATAGGAGATAT	420
Db	361	AGACTGTGGCCCTTCAAGTGGTCTTCTACTACTGTGATGAGATTCGGAAATATAGGAGATAT	420
OY	421	GGAGTGTGGTGGGAACCAACAAATCTCTACTGTGAAGAAGCAGAACTGGGAGATGGTG	480
Db	421	GGAGTGTGGTGGGAACCAACAAATCTCTACTGTGAAGAAGCAGAACTGGGAGATGGTG	480
OY	481	AGCCCAACAACAAGAAAGAAAGAGAGGACTCGTGGAGATCTATATCAGACAACAAG	540
Db	481	AGCCCAACAACAAGAAAGAAAGAGAGGACTCGTGGAGATCTATATCAGACAACAAG	540
OY	541	ATGCAAGCCAAATGAGACGATGACGCTTGCACAAACTAAAGAGCAGCCCTGTTCACAG	600
Db	541	ATGCAAGCCAAATGAGAAACGATGACGCTTGCACAAACTAAAGAGCAGCCCTGTTCACAG	600
OY	601	CTTCTTGGCAGCCGTGTGCATATGACGTGGCCATGGAGATGTGTAGAAATCATCAATAATC	660
Db	601	CTTCTTGGCAGCCGTGTGCATATGACGTGGCCATGGAGATGTGTAGAAATCATCAATAATC	660
OY	661	ACACCTGCACACTGTGATGTGGGTGACTATGAGGCCACAGTGCAGCTTGATTCACGTGG	720
Db	661	ACACCTGCACACTGTGATGTGGGTGACTATGAGGCCACAGTGCAGCTTGATTCACGTGG	720
OY	721	AGCCTTTGGAGGCCCGAGAGTGGGTACCATGACATGTACTACCCCTTTGGAAACTTCA	780
Db	721	AGCCTTTGGAGGCCCGAGAGTGGGTACCATGACATGTACTACCCCTTTGGAAACTTCA	780
OY	781	GCTTCAGCTCACAGTGTGCTTCAGCTGCCTGTAAGAAACAACCTTAACTGGGATTGAG	840
Db	781	GCTTCAGCTCACAGTGTGCTTCAGCTGCCTGTAAGAAACAACCTTAACTGGGATTGAG	840
OY	841	AAACCACTGTGGACCAATTTGGAACGTGTGCATCTCCAGAACCAACCTGTCAAGTATTC	900
Db	841	AAACCACTGTGGACCAATTTGGAACGTGTGCATCTCCAGAACCAACCTGTCAAGTATTC	900
OY	901	AGTGTGACCTCTTTCAGCACACGATTTGGGGATCTATGAAGCTGTAGCCATCCCTGGGCA	960
Db	901	AGTGTGACCTCTTTCAGCACACGATTTGGGGATCTATGAAGCTGTAGCCATCCCTGGGCA	960
OY	961	GCTTCACGTTTACTCTGTGCATGTACCTTATCTGCTCAGAGGAACCTAGTTAATTGGGA	1020
Db	961	GCTTCACGTTTACTCTGTGCATGTACCTTATCTGCTCAGAGGAACCTAGTTAATTGGGA	1020

Qy	1021	AGAGAAACCATTTTGATATATCGAATCTGTCAAATGCTAGTCCATATGTCAA	1080
Db	1021	AGAGAAACCATTTTGATATATCTGGAATCTGTCAAAATCTACTGCAATATGTCAA	1080
Qy	1081	AATTTGCAAAAGTTTCTCAATGATTAGAGGGGTGATTTAACTCCCTTCATTCAG	1140
Db	1081	AATTTGCAAAAGTTTCTCAATGATTAAAGAGGGGTGATTTAACTCCCTTCATTCAG	1140
Qy	1141	TGCGACTCATGTTACTGTCAATTCCTGGGTGGCATTTATCAATTTGGCTGGCAAGAGAT	1200
Db	1141	TGCGACTCATGTTACTGTCAATTCCTGGGTGGCATTTATCAATTTGGCTGGCAAGAGAT	1200
Qy	1201	TAAAAAAGGCAAGAAATCCAAAGAAAGTATGAAATGACCATATTAATCCGCTTGGTG	1260
Db	1201	TAAAAAAGGCAAGAAATCCAAAGAAAGTATGAAATGACCATATTAATCCGCTTGGTG	1260
Qy	1261	AAAGAAATTTCTTGGATACTAAATATCATAGATCCTTTAAATCCTTCATGAAAGTT	1320
Db	1261	AAAGAAATTTCTTGGATACTAAATATCATAGATCCTTTAAATCCTTCATGAAAGTT	1320
Qy	1321	TTTGTTGGTGGACCTCTCTAGCTAAACATGAAGTGTCTTCTTCAATCTGGAG	1380
Db	1321	TTTGTTGGTGGACCTCTCTAGCTAAACATGAAGTGTCTTCTTCAATCTGGAGAG	1380
Qy	1381	ATTTTACCCGACACAGATTCCTTCAGTCTTCATTTGCCTCATTTATCCCTCAAC	1440
Db	1381	ATTTTACCCGACCAAGAGTTCCTTCAGTCTTCATTTGCCTCATTTATCCCTCAAC	1440
Qy	1441	CCGACGCCACAGGTGTTATACGCTCAGCTTTTGTCTTTCTGAGAGAAACAAATA	1500
Db	1441	CCGACGCCACAGGGTGTATACACCTCAGCTTTTGTCTTTCTGAGAGAAACAAATA	1500
Qy	1501	GACCATTAAGGAAAGATTCATGCGAATATAAGTGGCTGACCTTGCTCTTGAC	1560
Db	1501	GACCATTAAGGAAAGATTCATGCGAATATAAGTGGCTGACCTTGCTCTTGAC	1560
Qy	1561	TCTTGTTCAGTTTCAATTCAGTCTGTACTTGATGACAGACATTTCAATGAAGTGC	1620
Db	1561	TCTTGTTCAGTTTCAATTCAGTCTGTACTTGATGACAGACATTTCAATGAAGTGC	1620
Qy	1621	AAATTTGATATATGTGAATATGACATGTTTCTTGACATCAATTTACGCTGTC	1680
Db	1621	AAATTTGATATATGTGAATATGACATGTTTCTTGACATCAATTTACGCTGTC	1680
Qy	1681	TTTGTATATCTGTGAGGTACCTTTATAGAAAGTTCAAAAAGTCAAGCTCTCCCTTC	1740
Db	1681	TTTGTATATCTGTGAGGTACCTTTATAGAAAGTCAAAAAGTCAAGCTCTCCCTTC	1740
Qy	1741	TTTCTAATCTCAGTGAAGTATGGGGTCTGCTCAAGTTGAAGAATCTTATTTGGACATG	1800
Db	1741	TTTCTAATCTCAGTGAAGTATGGGGTCTGCTCAAGTTGAAGAATCTTATTTGGACATG	1800
Qy	1801	TAGCCTGCGCTGTGAATTTGGACATCTTTTAACTGGCTTCAGGCTCCCAACCT	1860
Db	1801	TAGCCTGCGCTGTGAATTTGGACATCTTTTAACTGGCTTCAGGCTCCCAACCT	1860
Qy	1861	CTTGACGACCTCTCTTTTTCAGTTGGCTGACCTCCACACTGACATCTGATGAGTGCA	1920
Db	1861	CTTGACGACCTCTCTTTTTCAGTTGGCTGACCTCCACACTGACATCTGATGAGTGCA	1920
Qy	1921	AGCAAAAGGAGAAAGAAATAGCTGGGGCTTTTATGTTGGGGGTGTTTGCTGT	1980
Db	1921	AGCAAAAGGAGAAAGAAATAGCTGGGGCTTTTATGTTGGGGGTGTTTGCTGT	1980
Qy	1981	TTTCTTTATGAGACCATTCCTATTTCTTATATCAATTTTCTTTATACAGATATTA	2040
Db	1981	TTTCTTTATGAGACCATTCCTATTTCTTATATCAATTTTCTTTATACAGATATTA	2040
Qy	2041	TTTGTATGAAATATCTAGAAATCTTACGTGCAAGTGCATCTTTTATGATGTATAG	2100
Db	2041	TTTGTATGAAATATCTAGAAATCTTACGTGCAAGTGCATCTTTTATGATGTATAG	2100

Qy	2101	AAGGTTAAAAACAGTGGGAGAAATTCCTTGATTCACAAATGAAATGCTCTCCTTCCCTG	2160
Dy	2101 <td>AAGGTTAAAAACAGTGGGAGAAATTCCTTGATTCACAAATGAAATGCTCTCCTTCCCTG <td>2160</td> </td>	AAGGTTAAAAACAGTGGGAGAAATTCCTTGATTCACAAATGAAATGCTCTCCTTCCCTG <td>2160</td>	2160
Qy	2161 <td>CCCCCAGACGTTTATTCACCTTACGTAAGATTCACATATTCCTTTAAATTTCAATCAGGC</td> <td>2220</td>	CCCCCAGACGTTTATTCACCTTACGTAAGATTCACATATTCCTTTAAATTTCAATCAGGC	2220
Dy	2161 <td>CCCCCAGACGTTTATTCACCTTACGTAAGATTCACATATTCCTTTAAATTTCAATCAGGC</td> <td>2220</td>	CCCCCAGACGTTTATTCACCTTACGTAAGATTCACATATTCCTTTAAATTTCAATCAGGC	2220
Qy	2221 <td>CTGCCCTCAACCCCAACGGGGCCGGCAGACACACGTGGAAATTC</td> <td>2259</td>	CTGCCCTCAACCCCAACGGGGCCGGCAGACACACGTGGAAATTC	2259
Dy	2221 <td>CTGCCCTCAACCCCAACGGGGCCGGCAGACACACGTGGAAATTC</td> <td>2259</td>	CTGCCCTCAACCCCAACGGGGCCGGCAGACACACGTGGAAATTC	2259

```

1      RESULT 2
2      US-08-481-803-1
3      : Sequence 1, Application US/08481803
4      : Patent No. 5679346
5      : GENERAL INFORMATION:
6      : APPLICANT: Tedder, Thomas F. and Olivier G. Sperling
7      : TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYTE-ASSOCIATED CELL
8      : TITLE OF INVENTION: SURFACE PROTEIN
9      : NUMBER OF SEQUENCES: 1
10     : CORRESPONDENCE ADDRESS:
11     : ADDRESSEE: FISH & NEAVE
12     : STREET: 1251 Avenue of the Americas
13     : CITY: New York
14     : STATE: NY
15     : COUNTRY: USA
16     : ZIP: 10020
17     : COMPUTER READABLE FORM:
18     : MEDIUM TYPE: Floppy disk
19     : COMPUTER: IBM PC compatible
20     : OPERATING SYSTEM: PC-DOS/MS-DOS
21     : SOFTWARE: Patent In Release #1.0, Version #1.25
22     : CURRENT APPLICATION DATA:
23     : APPLICATION NUMBER: US/08/481,803
24     : FILING DATE:
25     : CLASSIFICATION: 424
26     : PRIOR APPLICATION DATA:
27     : APPLICATION NUMBER: US 08/215,366
28     : FILING DATE: 21-MAR-1994
29     : APPLICATION NUMBER: US 07/720,602
30     : FILING DATE: 25-JUN-1991
31     : PRIOR APPLICATION DATA:
32     : APPLICATION NUMBER: US 07/313,109
33     : FILING DATE: 21-FEB-1989
34     : ATTORNEY/AGENT INFORMATION:
35     : NAME: James F. Haley, Jr.
36     : REGISTRATION NUMBER: 27,794
37     : REFERENCE/DOCKET NUMBER: CG-101 CON
38     : TELECOMMUNICATION INFORMATION:
39     : TELEPHONE: (212) 596-9000
40     : TELEFAX: (212) 596-9090
41     : TELEX:
42     : INFORMATION FOR SEQ ID NO: 1:
43     : SEQUENCE CHARACTERISTICS:
44     : LENGTH: 2330 base pairs
45     : TYPE: nucleic acid
46     : STRANDEDNESS: single
47     : TOPOLOGY: linear
48     : MOLECULE TYPE: cDNA
49     : HYPOTHETICAL: NO
50     : ANTI-SENSE: NO
51     : FEATURE:
52     : NAME/KEY: CDS
53     : LOCATION: 53..1210
54     : US-08-481-803-1

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Query Match	92.4%	Score 2087.6;	DB 1;	Length 2330;
Best Local Similarity	98.5%;	Pred. No. 0;		
Matches 2161;	Conservative 0;	Mismatches 24;	Indels 9;	Gaps 5;

OY	44	CCCTTTGGCAGAGACCTTAGACACCTTGTGTGCTAACTCAAGAGGCTCATATGGGCTGTGAGAG	103
Dp	7	CTTTTGGGCAAGAGACCTTAGACACCTTGTGTGCTAACTCAAGAGGCTCATATGGGCTGTGAGAG	66
OY	104	AACCTAGAGAGGACCAACCAAGGCATGATATTTTTCATATGGAAATGTTCAGAGCACCCGAG	163
Dp	67	AACCTAGAGAGGACCAACCAAGGCATGATATTTTTCATATGGAAATGTTCAGAGCACCCGAG	128
OY	154	GGACCTTATGGAACATCTTTCAAGTTGTGGGGGTGACACATGCTCTGTGTGCAATTTTCGTGGC	223
Dp	127	GGACCTTATGGAACATCTTTCAAGTTGTGGGGGTGACACATGCTCTGTGTGCAATTTTCGTGGC	186
OY	224	ACATCATGGAACCTTACTGTCTGGACTTACCATTTATCTGAAAACCCATGAACTGGCAAG	283
Dp	187	ACATCATGGAACCCGACTGTCTGGACTTACCATTTATCTGAAAACCCATGAACTGGCAAG	246
OY	284	GGCTTAGAGATTTCTGGCCGAGACATTTACAGATTTTGTGGTCCATACAAAACAAAGCGGGA	343
Dp	247	GGCTTAGAGATTTCTGGCCGAGACATTTACAGATTTTGTGGTCCATACAAAACAAAGCGGGA	306
OY	344	AATTGAGATATCTGGAGAGACTGTGCCCTTTCAGTCTGTTTCTTACTACTGATAGGAATCCG	403
Dp	307	AATTGAGATATCTGGAGAGACTGTGCCCTTTCAGTCTGTTTCTTACTACTGATAGGAATCCG	366
OY	404	GAGATAGAGGAGATATGAGACGTGGGTGGAGACCAACAAATCTCTCATAGAGAGCAGA	463
Dp	367	GAGATATAGGAGAGATATGAGACGTGGGTGGAGACCAACAAATCTCTCATAGAGAGCAGA	426
OY	464	GAACTGGGGCAATGTGTAGGCCCAACACAAAGAAACAAAGAGAGACTGCTGGAGATCTA	523
Dp	427	GAACTGGGGCAATGTGTAGGCCCAACACAAAGAAACAAAGAGAGACTGCTGGAGATCTA	486
OY	524	TATCAAGAGAAACAAGATGAGGCAATGGAAGATGAGCGCTGCCACAACCAATAAAGGC	583
Dp	487	TATCAAGAGAAACAAGATGAGGCAATGGAAGATGAGCGCTGCCACAACCAATAAAGGC	546
OY	584	AGCCCTCTGTACACAGCTTCTGCCAGCCCTGTGTCATGAGTGGCCATGAGAAATGTGT	643
Dp	547	AGCCCTCTGTACACAGCTTCTGCCAGCCCTGTGTCATGAGTGGCCATGAGAAATGTGT	606
OY	644	AGAAATCATCATATATCACAACCTTGCAACTGTGATGTGGGGTACTATATGGGCCCAAGTCTCA	703
Dp	607	AGAAATCATCATATATTAACACTTGCAACTGTGATGTGGGGTACTATATGGGCCCAAGTCTCA	666
OY	704	GCTTGTGATTTAGTGTGAGGCTTTTGGAGGCCCCGAGACTGGGGTACCATGTGAGCTGTCTCA	763
Dp	667	GCTTGTGATTTAGTGTGAGGCTTTTGGAGGCCCCGAGACTGGGGTACCATGTGAGCTGTCTCA	726
OY	764	CCCCCTTTGGAACCTTCAGCTTCAGCTCACAAGTGTGCCCTTCAGCTGCTCTGAGGAACAA	823
Dp	727	CCCCCTTTGGAACCTTCAGCTTCAGCTCACAAGTGTGCCCTTCAGCTGCTCTGAGGAACAA	786
OY	824	CTTAACTGTGGATTTAGAGAAACCACTGTGACCAATTTTGGAACTGTCTCATCTCCAGAAC	883
Dp	787	CTTAACTGTGGATTTAGAGAAACCACTGTGACCAATTTTGGAACTGTCTCATCTCCAGAAC	846
OY	884	AACCGTCAACTGTATTCAGTGTGAGGCTCTATACAGCAACCAATTTGGGGATTCATATGAATG	943
Dp	847	AACCTGTCAACTGTATTCAGTGTGAGGCTCTATACAGCAACCAATTTGGGGATTCATATGAATG	906
OY	944	TAGGCATCCCTGTGCCAGCTTCAGCTTACTCTGCAATGTACCTTCACTCTGCTCAGAAAG	1000
Dp	907	TAGGCATCCCTGTGCCAGCTTCAGCTTACTCTGCAATGTACCTTCACTCTGCTCAGAAAG	966
OY	1004	AACCTGAGTTAATTGGGAGAGAAACCAATTTGTGAATCATCTGGAATCTGTGTCAATTC	1060
Dp	967	AACCTGAGTTAATTGGGAGAGAAACCAATTTGTGAATCATCTGGAATCTGTGTCAATTC	1022
OY	1064	TAGTGCATAATGTCAAAAAATTTGGCAAAAGTTTCTCATATTAAGAGAGGTCATTAATA	1120
Dp	1027	TAGTGCATAATGTCAAAAAATTTGGCAAAAGTTTCTCATATTAAGAGAGGTCATTAATA	1080
OY	1124	CCCCCTCTCATTTCAATGGCAGCATAGTTACTGCAATTTCTGTGGGTGGCATTTAAT	1180

1124	CCCCCTCTTCATTCAGAGGAGTCATGGTTACTGCAATTCCTGTGGGTGSCATTATTCAT	118
1027	TAGTGCATATATGTCAAAAATTTGCACAAAAGTTTCTCATGATTAAAGGAGCGCTATTATATA	108
1004	TAGTGCATATATGTCAAAAATTTGCACAAAAGTTTCTCATGATTAAAGGAGCGCTATTATATA	112
97	TAGTGCATATATGTCAAAAATTTGCACAAAAGTTTCTCATGATTAAAGGAGCGCTATTATATA	112



OY	224	ACATCATGGAACCTACAGTGGAGCTTACCATTTATCTGAAAAAACCATGAACTGGCAAG	283
Db	187	ACATCATGGAACCCACAGCTGTGGACTTTCACATTTATCTGAAAAAACCATGAACTGGCAAG	246
OY	284	GGCTAGAAAGATTCTGGCCAGACAATTCACACAGATTATAGTCCCATACAAACAGGCGGA	343
Db	247	GGCTAGAAAGATTCTGGCCAGACANATTACACAGATTATAGTGGCCATACAAACAGGCGGA	306
OY	344	AATTGAGTATCTGGAGAAGACTCGCCCTTCAGTCCGTTCTTACTAGTGAATAGCAATCCG	403
Db	307	AATTGAGTATCTGGAGAAGACTCGCCCTTCAGTCCGTTCTTACTAGTGAATAGCAATCCG	366
OY	404	GAAGATAGAGAGAAATATGAGCTGGGTGGGAACCAACAATCTCTCATCTGAAGAAGCAGA	463
Db	367	GAAGATAGAGAGAAATATGAGCTGGGTGGGAACCAACAATCTCTCATCTGAAGAAGCAGA	426
OY	464	GAACGGGGAGATGTGTGAGCCCAACAAGAAAGAAACAAGAGAGACTGGGTGGAGATCTGA	523
Db	427	GAACGGGGAGATGTGTGAGCCCAACAAGAAAGAAACAAGAGAGACTGGGTGGAGATCTGA	486
OY	524	TATCAAGAGAAACAAGATGACAGCAATGGAACGATGACGCCCTGCCACAACTAAAGGC	583
Db	487	TATCAAGAGAAACAAGATGAGGCAATGGAACGATGACGCCCTGCCACAACTAAAGGC	546
OY	584	AGCCCTCTGTTACACAGCTTCTTGCCAGCCCTGTGTCATGCAAGTGGCCATGAGAAATGTGT	643
Db	547	AGCCCTCTGTTACACAGCTTCTTGCCAGCCCTGTGTCATGCAAGTGGCCATGAGAAATGTGT	606
OY	644	AGAAATCATCATATATACACACCTGGCAACCTGTGATGTGGGTACTATAGGGCCCCAGTGTCA	703
Db	607	AGAAATCATCATATATATACACCTGTGCAACTGTGATGTGGGTACTATAGGGCCCCAGTGTCA	666
OY	704	GCATTGTGATTTAGTGTGAGCCCTTTGGAGGCCCCAGACAGCTGGGATCCATGGACTGTACTCA	763
Db	667	GCATTGTGATTTAGTGTGAGCCCTTTGGAGGCCCCAGACAGCTGGGATCCATGGACTGTACTCA	726
OY	764	CCCCCTTGGAAACTTTCAGCTTCAGCTCACAGTGTGCTTACAGCTGCTGTGAAGAACAA	823
Db	727	CCCCCTTGGAAACTTTCAGCTTCAGCTCACAGTGTGCTTACAGCTGCTGTGAAGAACAA	786
OY	824	CTTTACAGTGGGATTCGAACAAACCAACCTGTGACCATTTGGAACTGGTCAATCTCCAGAAC	883
Db	787	CTTTACAGTGGGATTCGAACAAACCAACCTGTGACCATTTGGAACTGGTCAATCTCCAGAAC	846
OY	884	AACCTGTCAAGTGTGATGAGTGTGAGCCCTCATGACACACAGATTTTGGGATCATGAACTG	943
Db	847	AACCTGTCAAGTGTGATGAGTGTGAGCCCTCATGACACACAGATTTTGGGATCATGAACTG	906
OY	944	TAGCCATCCCTGGCCAGCTTTCAGCTTACCTGTGCATGTACCTTCATCTGCTCAGAAAG	1003
Db	907	TAGCCATCCCTGGCCAGCTTTCAGCTTACCTGTGCATGTACCTTCATCTGCTCAGAAAG	966
OY	1004	AACGTAGTTAATTGGGAAGAAACCAATTTGTGAATCATCTGGAATCTGGTCAAAATCC	1063
Db	967	AACGTAGTTAATTGGGAAGAAACCAATTTGTGAATCATCTGGAATCTGGTCAAAATCC	1026
OY	1064	TAGTTCCAATATGTCAAAAAATTTGGCAAAAGATTTCATAATGATTTAAAGAGAGGTGATTTATA	1123
Db	1027	TAGTTCCAATATGTCAAAAAATTTGGCAAAAGATTTCATAATGATTTAAAGAGAGGTGATTTATA	1086
OY	1124	CCCCCTCTTCAATTCAGTGGCAGTTCATGTGTTACTGCAATCTCTGAGGTGGCATTTATCAT	1183
Db	1087	CCCCCTCTTCAATTCAGTGGCAGTTCATGTGTTACTGCAATCTCTGAGGTGGCATTTATCAT	1146
OY	1184	TTGGCTGTGCAAGAGATTTAAAAAAGGCAAGAAATCCAGAGAAAGTATGAAATGACCCATA	1243
Db	1147	TTGGCTGTGCAAGAGATTTAAAAAAGGCAAGAAATCCAGAGAAAGTATGAAATGACCCATA	1206
OY	1244	TTTAAATGGCCCTTGGTGAAGAAATTTCTTGGAAATCTGATTAATGATGATTCCTTTTAAA	1303
Db	1207	TTTAAATGGCCCTTGGTGAAGAAATTTCTTGGAAATCTGATTAATGATGATTCCTTTTAAA	1266
OY	1304	TCTCTTCATGAAAGTTTGTGTGTGGCCACTCTCAGCTCAACATGAAAGTGTG-TTCC	1362

Dd	1267	TCTCTCCATGGAACGGTTTGTGTGTGTGGCACCTCCTCAAGTCAAACACTGAAAGTGCTGTTC	1326
Oy	1363	TTTCAGTGCATCTGGGAGAATTCTTACCGCCAGCAACAGTTCCCTTACCTTTCATATTTCCGCC	1422
Dd	1337	TTCACTGCATCTGGGAGATTCTTACTGACCAACAATCTCTTCACTTTCATTTACCC	1386
Oy	1423	CTCATTTATCCCTCAACCCCACGACCACAGGTGTTTATACAGCTACGTTTTGTCTTTT	1483
Dd	1387	CTCATTTATCCCTCAACCCCCACAGGTGTTTATACAGCTACGTTTTGTCTTTT	1446
Oy	1483	CTGAGGAGAAAACAATAAGACAT- AAGGGAAGGATTCTGTGGAAATTAAGAATGGCT	1544
Dd	1447	CTGAGGAGAAAACAATAAGACATAAAGGGAAGGAAAGATTCTGTGGAAATTAAGAATGGCT	1506
Oy	1542	GACCTTGGCTCTTCTCTACACCTCTGTTTTCAGTTTCAAATTCAGTGCCTGTAAGATGACAG	1600
Dd	1507	GACCTTGGCTCTTCTCTACACCTCTGTTTTCAGTTTCAAATTCAGTGCCTGTAAGATGACAG	1566
Oy	1602	ACACTTCTAATAATGAAGCAAAATTTGATACATATGTAATATGAGTACAGTTTCTTGA	1661
Dd	1567	ACACTTCTAATAATGAAGCAAAATTTGATACATATGTAATATGAGTACAGTTTCTTGA	1626
Oy	1662	GATCAAATTTACGTGCTTCTGTATACGTGTGAGGTACACTCTTATAGAAATTCANA	1721
Dd	1627	GATCAAATTTGCGTCTGCTCTGTATATAC- GTGAGAGTACACTCT-----ATGAAGTCNA	1680
Oy	1722	AAGTCTACGCTCTCTCTTCTTCTAACCTCACTCAAGGAAGTAATGGGGTCTGCTCAAGTTCA	1788
Dd	1681	AAGTCTACGCTCTCTCTTCTTCTAACCTCAAGGAAGTAATGGGGTCTGCTCAAGTTCA	1746
Oy	1782	AAGAGTCCATTTTACAGTATAGCTCGCCCTCTGTAAATTTGACCAATTCCTATTTAACTGG	1841
Dd	1741	AAGAGTCCATTTTACAGTATAGCTCGCCCTCTGTGTGAATTTGACCAATTCCTATTTAACTGG	1800
Oy	1842	CTTCAGGCTCTCCCACTCTTCTACGACCACTCTCTTTTACGTGGCTGACTTCCACACC	1901
Dd	1801	CTTCA- GCGTCCCAACCTCTCTACGACCACTCTCTTTTACGTGGCTGACTTCCACACC	1859
Oy	1902	TAGACATCAGAGTAGTGGCAAGCAAAAGSAGAGAAGAGAAATAGCCTCGCGGGTTTTTTT	1966
Dd	1860	TAGACATCAGAGTAGTGGCAAGCAAAAGSAGAGAAGAGAAATAGCCTCGCTGTTTTTT	1919
Oy	1962	AGTTTGGGGGTTTGGCTGTTTCCCTTTTATGAGACCCATTCCTATTTCTTATAGTCAATGT	2021
Dd	1920	AGTTTGGGGGTTTGGCTGTTTCCCTTTTATGAGACCCATTCCTATTTCTTATAGTCAATGT	1979
Oy	2022	TTCTTTTATCAGATATTATTATGTAAGAAAATCATCACTGAATGCTAGTSCGAAGTGACA	2081
Dd	1980	TTCTTTTATCAGATATTATTATGTAAGAAAATCATCACTGAATGCTAGTSCGAAGTGACA	2039
Oy	2082	TCTCTTGAATGTCATATGGAAGGATTAAACAGCTGAGAAANTCCCTTATTCACAAATGA	2144
Dd	2040	TCTCTTGAATGTCATATGGAAGGATTAAACAGCTGAGAAANTCCCTTATTCACAAATGA	2099
Oy	2142	AATGCTCTCTTTCCCTCGCCCCAGAACCTTTATCAGTACCTAGATTCTACATATTTC	2201
Dd	2100	AATGCTCTCTTTCCCTCGCCCCAGAACCTTTTATCAGTACCTAGATTCTACATATTTC	2159
Oy	2202	TTTAAATTCATCTCAGGCGCTCCCTCAACCCAC	2235
Dd	2160	TTTAAATTCATCTCAGGCGCTCCCTCAACCCAC	2193
 RESULT 4 US-08-340-539A-1 ; Sequence 1, Application US/08340539A ; Patent No. 5808025 ; GENERAL INFORMATION: ; APPLICANT: Tedder, Thomas F. ; APPLICANT: Kansas, Geoffrey S. ; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS ; ; BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION			

Query	Match	Similarity	98.5%	Score	2087.6	DB 1	Length	2330
Best Local	Similarity	98.5%	Fred	No. 0				
Matches	2161	Conservative	0	Mismatches	24	Indels	9	Gaps
QY	44	CCCTTTGCCAAGACCTGAGACCCCTTGTGCAAGTCAAGAGGCTCAATGGCGTGCAGAG	103					
Db	7	CCTTTGGGGAAGACCTGAGACCCCTTGTGCAAGTCAAGAGGCTCAATGGCGTGCAGAG	66					
QY	104	AACATAAGAGAAGCAACCAAGCAAAAGCCATATATTTTCATGTGAATATGTCAGAGCACCCAGAG	163					
Db	67	AACATAAGAGAAGCAACCAAGCAAAAGCCATATATTTTCATGTGAATATGTCAGAGCACCCAGAG	126					
QY	164	GGACTATATGGACATCTTCAAGTTGTGGGGGTGGACAACTCTCTGTGTGATTTCTGTGC	223					
Db	127	GGACTATATGAACATCTTCAAGTTGTGGGGGTGGACAACTCTCTGTGTGATTTCTGTGC	186					
QY	224	ACATCATGGAACTCTACTGCTGACTTACCAATTATTCGAAAAAACCATGAATGCGCAAG	283					
Db	187	ACATCATGGAACTCTACTGCTGACTTACCAATTATTCGAAAAAACCATGAATGCGCAAG	246					
QY	284	GGCTGAAGAATTCCTCCCGAGACAAATTACACAGATTTTAGTTGCCATTCACAAACAGAGCGGA	343					
Db	247	GGCTGAAGAATTCCTCCCGAGACAAATTACACAGATTTTAGTTGCCATTCACAAACAGAGCGGA	306					
QY	344	AATTAGATATCTGAGAAGACTCTGCCCTTCATCTGCTTCTACTACTGGATAGCAATCGG	403					
Db	307	AATTAGATATCTGAGAAGACTCTGCCCTTCATCTGCTTCTACTACTGGATAGCAATCGG	366					
QY	404	GAGATATAGAGCAATATGAGACGTGGGGTGGGAACCAACAATCTCTCACTGAAGAAGCAGA	463					
Db	367	GAGATATAGAGCAATATGAGACGTGGGGTGGGAACCAACAATCTCTCACTGAAGAAGCAGA	426					
QY	464	GAACTGGGAGATGCTGAGGCCCAACAACAAGAAGAAACAAGAGACTGCTGAGGATCTA	523					

D	427	GAACCTGGGAGATGGTGGAGCCCAACAAAGAAAGAACAGAGGAGCACTGCTGGAGATCTA	486
OY	524	TATCAAGAGAAACAACAGATGAGGCAAAATGAAACGATGAGCGCTCCCAACTAACTAAAGC	583
D	487	TATCAAGAGAAACAAGATGAGGCAAAATGAAACGATGAGCGCTCCCAACTAAAGAGC	546
OY	584	AACCTCTGTTTACACAGCTTCTGGCCAGCGCTGTCATCATGTGGCCATGAGAAATGTG	643
D	547	AACCTCTGTTTACACAGCTTCTGGCCAGCGCTGTCATCATGTGGCCATGAGAAATGTG	606
OY	644	AGAAATCATCATATATATACACCTGCAACCTGTATGTGGGTACTATGGCCCAAGTGTCA	703
D	607	AGAAATCATCATATATATATACACCTGCAACCTGTATGTGGGTACTATGGCCCAAGTGTCA	666
OY	704	GCTTGTGATTCAGTGTGAGCGTTTGGAGGCCCCAGAGCTGGGTACCAATGAGACTGTCTCA	763
D	667	GTTTGTGATTCAGTGTGAGCGTTTGGAGGCCCCAGAGCTGGGTACCAATGAGACTGTCTCA	726
OY	764	CCCCCTTGGAAACCTCAAGCTCAAGCTCAACAGTGTCCCTTACGCTGCTCTGAAAGAACAA	823
D	727	CCCCCTTGGAAACCTCAAGCTCAAGCTCAACAGTGTCCCTTACGCTGCTCTGAAAGAACAA	786
OY	824	CTTAACTGGGATTTGAAGAAACCAGCTGTGAGCAATTTTGAAGCTGGTCATCTCCAAAC	883
D	787	CTTAACTGGGATTTGAAGAAACCAGCTGTGAGCAATTTTGAAGCTGGTCATCTCCAAAC	846
OY	884	AACCTGTCAAGTGAATTCAGTGTGAGCGCTTATCAGCACACAGATTTGGGATCATGAAGTG	943
D	847	AACCTGTCAAGTGAATTCAGTGTGAGCGCTTATCAGCACACAGATTTGGGATCATGAAGTG	906
OY	944	TAGCCATCCCTGGCCAGGCTTACGTTTACCTGTGCATGTACCTTATGCTCGTCAAGAG	1003
D	907	TAGCCATCCCTGGCCAGGCTTACGTTTACCTGTGCATGTACCTTATGCTCGTCAAGAG	966
OY	1004	AACCTGATTAATTTGGAGAGAAAGAAACCATTTTGAATCATCTGGAATCTGGTCAAAATCC	1063
D	967	AACCTGATTAATTTGGAGAGAAAGAAACCATTTTGAATCATCTGGAATCTGGTCAAAATCC	1026
OY	1064	TAGTCCAAATATGTCAAAATTTGAGCAAAAGTTCTCAATGATTAAGAGAGGTATTATA	1123
D	1027	TAGTCCAAATATGTCAAAATTTGAGCAAAAGTTCTCAATGATTAAGAGAGGTATTATA	1086
OY	1124	CCCCCTTTCATTCAGTGTGACAGTCAATGTTTACTGCATTTCTGTGGTGGCAATTATCAT	1183
D	1087	CCCCCTTTCATTCAGTGTGACAGTCAATGTTTACTGCATTTCTGTGGTGGCAATTATCAT	1146
OY	1184	TTGGCTGGAGAGGAGATTTAAAAAAGCCAGAAATCCAGAGAAATATATGATGACCATTA	1243
D	1147	TTGGCTGGAGAGGAGATTTAAAAAAGCCAGAAATCCAGAGAAATATATGATGACCATTA	1206
OY	1244	TTTAAATCGCCCTTGCTGCAAGAAATTTCTTGAATCTTAAAAATCATGAGATCCCTTAAA	1303
D	1207	TTTAAATCGCCCTTGCTGCAAGAAATTTCTTGAATCTTAAAAATCATGAGATCCCTTAAA	1266
OY	1304	TCCCTTCATGAAAGGTTTGTGTGTGGGCAACCTCCAGCTCAACATGAAAGTGTG -TTCC	1362
D	1267	TCCCTTCATGAAAGGTTTGTGTGTGGGCAACCTCCAGCTCAACATGAAAGTGTGTTC	1326
OY	1363	TTTCACTGCATCTGGGAGATTTCTACCCAGCAACAGTTCCTTCAGCTTCATTTGCGCC	1422
D	1327	TTTCACTGCATCTGGGAGATTTCTACCCAGCAACAGTTCCTTCAGCTTCATTTGCGCC	1386
OY	1423	CTCATTTATCCCTCAACCCCGACCCCAACAGGTTTATATACAGCTCACTTTTGTCTTTT	1482
D	1387	CTCATTTATCCCTCAACCCCGACCCCAACAGGTTTATATACAGCTCACTTTTGTCTTTT	1446
OY	1483	CTGAGGAGAAACAATATAGACAT -AAGGAGAAAGATTCATGTGGATTTAAAGATGGCT	1541
D	1447	CTGAGGAGAAACAATATAGACAT -AAGGAGAAAGATTCATGTGGATTTAAAGATGGCT	1506
OY	1542	GACTTTCCTTCTTCTGACTCTTGTTTCAAGTTCAATCATGCTGTACTGTATGACAG	1601



Db	1507	GACITTCGCTCTTTCCTGACCTGCTGTTTACAGTTTCAATTCACATGCTGCTGATGATGACAG	1566
Qy	1602	ACACCTTCAATGAAGTGCACAAATTTATATACATATGTGAATATAGACTACAGTTTCTTGCA	1661
Db	1567	ACACTTCCTAAATGAAGTGCACAAATTTATATACATATGGAATATAGACTACAGTTTCTTGCA	1626
Qy	1662	GATCAAAATTCACGTGCTGCTTCTGTATACGTGAGAGTACACTCTCTTATGAAGTTCCANA	1721
Db	1627	GATCAAAATTCGCGTCTCTTCTGTATAC- GTGAGAGTACACTCT- ----ATGAAGTCAA	1680
Qy	1722	AAGTCACGCT	1781
Db	1681	AAGTCACGCT	1740
Qy	1782	AAGAGTCCTATTTTGACACTGTAGCCCTGCGCTGTGTGAATTTGAGACCATCTTATTAACGTG	1841
Db	1741	AAGAGTCCTATTTTGACACTGTAGCCCTGCGCTGTGTGAATTTGAGACCATCTTATTAACGTG	1800
Qy	1842	CTTCAGGCGCTCCACCT	1901
Db	1801	CTTCAC- GCGTCCGACCT	1859
Qy	1902	TAGACATCTCATGTAGTGCACAGCAAAAGAGAGAGAGAAATPACCTGCGCGGTTTTTTTT	1961
Db	1860	TAGACATCTCATGTAGTGCACAGCAAAAGAGAGAGAAATPACCTGCGCGTGTTTTTT	1919
Qy	1962	AGTTTGGGGGTTTTTCTGTTTCT	2021
Db	1920	AGTTTGGGGGTTTTTCTGTTTCT	1979
Qy	2022	TTCCTTTATCAGCATATTTATTTAGTAAAGAAACATCATCTGAATTTGTACTGCAAGTACA	2081
Db	1980	TTCCTTTATCAGCATATTTATTTAGTAAAGAAACATCATCTGAATTTGTACTGCAAGTACA	2039
Qy	2082	TCTCTTTGATGTCAATATGAGAAAGTTTAAACAGGTGAGAAATTCCTTGATTTCAATATGA	2141
Db	2040	TCTCTTTGATGTCAATATGAGAAAGTTTAAACAGGTGAGAAATTCCTTGATTTCAATATGA	2099
Qy	2142	AATGCT	2201
Db	2100	AATGCT	2159
Qy	2202	TTTATATTTTCATCTCAGAGCCTCCCTCAACCCAC	2235
Db	2160	TTTATATTTTCATCTCAGAGCCTCCCTCAACCCAC	2193
RESULT 5			
US-08-461-592B-1			
: Sequence 1, Application US/08461592B			
: Patent No. 5834425			
: GENERAL INFORMATION:			
: APPLICANT: Tedder, Thomas F.			
: APPLICANT: Kansas, Geoffrey S.			
: TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS			
: NUMBER OF SEQUENCES: 11			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Weingarten, Schurjin, Gagnebin & Hayes			
: STREET: Ten Post Office Square			
: CITY: Boston			
: STATE: MA			
: COUNTRY: USA			
: ZIP: 02109			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: Patentin Release #1.0, Version #1.25			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/461,592B			
: FILING DATE:			
: CLASSIFICATION: 514			

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/340,539  
 FILING DATE: 16-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/008,459  
 FILING DATE: 25-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr.,  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: CG-104  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 596-9000  
 TELEFAX: (212) 596-9090  
 TEXEL: 14-8367  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2330 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 53..1210  
 US-08-461-592B-1

Query Match	92.48;	Score 2087.6;	DB 2;	Length 2330;
Best Local Similarity	98.58;	Pred. No. 0;		
Matches 2161; Conservative	0;	Mismatches 24;	Indels 9;	Gaps 5

QY	44	CCCTTTGGCAGAGACCTGAGACCCCTTGCGTAACTCAAGAGCCCTCATATGGCTCCCAAG	1.03
Db	7	CCCTTTGGCAGAGACCTGAGACCCCTTGCGTAACTCAAGAGCCCTCATATGGCTCCCAAG	66
QY	104	AACTAGAGAAAGGACCAAGCAAGCCATGATATTTCATGTGAATGTCAAGCACCCAGAG	1.63
Db	67	AACTAGAGAAAGGACCAAGCAAGCCATGATATTTCATGTGAATGTCAAGCACCCAGAG	1.28
QY	164	GGACCTTATGSAACATCTTCAAGTTGTGGGGGTGACAAATGCTCTGTTGTGATTTCTGGC	2.23
Db	127	GGACCTTATGSAACATCTTCAAGTTGTGGGGGTGACAAATGCTCTGTTGTGATTTCTGGC	1.88
QY	224	ACATCATGGAACCTACTGCTGCTGAGATTTCACATATTTCGAAAAACCCATGAACTGGCAAG	2.83
Db	187	ACATCATGGAACCTACTGCTGCTGAGATTTCACATATTTCGAAAAACCCATGAACTGGCAAG	2.46
QY	284	GGCTAGAAAGATTTCGCCGAGACATTTACACAGATTTAGTGGCTACCAAAACAGGCGGA	3.43
Db	247	GGCTAGAAAGATTTCGCCGAGACATTTACACAGATTTAGTGGCTACCAAAACAGGCGGA	3.08
QY	344	AATTGAGTATCTGGAGAGACTTGCCCTTCAGTCTGTTACTACTGATAGGAATCCG	4.03
Db	307	AATTGAGTATCTGGAGAGACTTGCCCTTCAGTCTGTTACTACTGATAGGAATCCG	3.66
QY	404	GAAATATAGAGAGATTATGAGAGTGGGTGGGAGCAACAAATCTCTCACTAACAAGCAGA	4.53
Db	367	GAAATATAGAGAGATTATGAGAGTGGGTGGGAGCAACAAATCTCTCACTAACAAGCAGA	4.26
QY	464	GAACTGGGAGATGGTAGGCCCAACACACAGAAAGAACAGAGAGACTGCGTGAGATCTA	5.23
Db	427	GAACTGGGAGATGGTAGGCCCAACACACAGAAAGAACAGAGAGACTGCGTGAGATCTA	4.86
QY	524	TATCAAGAGAAACAAGATGACGCAAAATGGAACGATGACGCTGCCACAACCTAAAGGC	5.83
Db	487	TATCAAGAGAAACAAGATGACGCAAAATGGAACGATGACGCTGCCACAACCTAAAGGC	5.46
QY	584	AGGCGCTCTGTACACAGCTTCTTGCCAGCCCTGTGTCAATGCAATGGCCATGGACAATCTCT	6.43
Db	547	AGGCGCTCTGTACACAGCTTCTTGCCAGCCCTGTGTCAATGCAATGGCCATGGACAATCTGT	6.06



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Db 121 gcaaaagccatgatacttccatgaaatgctcagagcaccagagggactatgaaacatct 180
Oy 181 TCAAGTTGGGGGAGCAATGCTCTGTGATTTCTGGACATCATGGAACCTACT 240
Db 181 tcaagttgvgggatgagcaaatgctcgtctgtaattctccgtgcaacatcaatggaactcct 240
Oy 241 GCTGGACTTACCAATTAATCTGAAAAAACCCATGAACCTGCAAAAGGGCTGAAGATTCTGCC 300
Db 241 gctggacttaacatattcttgaaaaccatgaaactgcaaaaggctagaagatctctgc 300
Oy 301 GAGACAATTACACAGATTAACTTGGCCATACAAACAGCGGAAATTGAGTAATCTGAGCA 360
Db 301 gagaacaatacagatttagtgcatacaaaaacaaagcggaattgagtaatcvgaga 360
Oy 361 AGACTCTCCCTTCAGTGTGCTTACTACTGATAGTAAGTAATCCGGAAAGTATGAGGAATAT 420
Db 361 agactctcccttcagttcgttcttactactgtaagtaacccggaatagaggaatatac 420
Oy 421 GGACGTGGGTGGGAACCAACAATCTCAGTGAAGAGAGAGAACTGCGAGATGGTG 480
Db 421 ggaagtgvggvggaaacaaatctctcactgaaagaagcagaagactcgggagagatg 480
Oy 481 AGCCCAACACAGAGAAGAGAGAGAGACTGCGTGGAGATCTATATCAAGAGAAACAAG 540
Db 481 agcccaacaacagaagaagaagaagagactcgvgagatctataatcaagaagaacaag 540
Oy 541 ATGCAGGAATGGAACATGACGCTTCGCACAAACTAAAGGACGCTCTGTTACACAG 600
Db 541 atgagagaaatggaacagatgacgcttcgcacaaactaaaggcctctgttacaag 600
Oy 601 CTCTTGGCACCCCTGGTGCATGACAGTGGCCATGAGAAATGTAATTCATCAATAATC 660
Db 601 ctcttgcacagcctgggtgcatacgacatgagcaatgagaaatgtaaaatcaatcaatc 660
Oy 661 ACACCTGCACACTGTGATGATGGGTACTATGAGGCCACAGTGCAGCTTGTGATTCAGTGTG 720
Db 661 acacctgcaactgtaatgctgaggtactatacggccccagtgtaagcttgatctcagtg 720
Oy 721 AGCCTTGGAGGCCCCAGAGCTGGTNCATGAGACTGATACACCCCTTGGAAACTTCA 780
Db 721 agccttggagggcccaagactggtgtactacatgtaaccccttggaaacttca 780
Oy 781 GCTTCAGCTCAGTGTGCTTCACTGCTTCAGCTGCTTCGAAGCAACAATTAATGGAAG 840
Db 781 gcttcagctcagatgctgcttccacgctgctctgaaagaaacaaacttaacttgatgag 840
Oy 841 AAACCACTGTGGAACCAATTTGGAACCTGTCATTCAGAACCAACCTGCAAGTGAATTC 900
Db 841 aaaccaactgtggaacatttggaaactgtatctccagaaaccaacactc----- 890
Oy 901 AGTGTGAGCCTCTATCAGACCAATTTGGGATCATGAATCTGATGCCATCCCTGGCCA 960
Db 901 agtgtgagcctctatcagaccagaatttgggataatgtaactgtaacatcccttggcca 960
Oy 961 GCTTCAGCTTACCTTCATGATACCTTCATCTGCTCAGAGGAACCTGATTAATGGGA 1020
Db 961 gcttcagcttacccttcgcaatgtaactcctcagcagaagaaactgagtaaatgagga 1020
Oy 1021 AGAAGAAAACCAATTTGTAATCATCTGGAATCTGTCAAATCTAGTCCAATATGTCAA 1080
Db 1021 agaagaaaacacattgtgaatcatctgtaactcgtgtcaaatccctcagtaataatgtaaa 1080
Oy 1081 AATTGGACAAAATTTCTCAATGATTAAGAGGGTGAATTATACCCCTCTTCATTCAG 1140
Db 1081 aattggacaaaatgttctcaatgattaaaggaggtgtaataaaccctctctcatcag 1140
Oy 1141 TGGCAGTACGTTACTGATCTCTGCTGGTGGCATTTATATATTTGCTGCAAGAGAT 1200
Db 1141 tggcagatcgttactgactctcctggtggcatcttctggtgcaatcttgcctgcaagagat 1200
Oy 1201 TAAAAAAGGACAGAAATCAAGAGAACTATGAATGACCAATATTAATTCGCCCTTGGTGC 1260

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Db 1191 taaaaaagcgcaagaatcccaagaagatgataatgacccaatataatcgcccttgg 1250
Oy 1261 AAGAATAATTTGGAAATACATAAATATCATGATGATCCTTTAAATCCTTCATGAAGATT 1320
Db 1261 aagaataatcttggaaatacctaa----- 1274
Oy 1331 TWTGCTGGTGGACCTCCTACGTCAAACATGAAGTGTGTCCTTCAGTGCATCTGGGAAG 1380
Db 1275 ----- 1274
Oy 1381 ATTTACCCGACACAGATTCTTCAGCTTCATTTGCCCTCATTTATCCCTCAACC 1440
Db 1275 ----- 1274
Oy 1441 CCCAGCCACAGGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAAACAAATTA 1500
Db 1275 -----agtgatataaagctcagcttcttcttcttctgaggaagaacaataaa 1324
Oy 1501 GACCAATAAGGGAAGAAAGATTCATGTAATATTAAGATGCTGACTTTCCTTTCAGTGC 1560
Db 1325 gacctaaaggaagaagatctcatgtaataataaagaatgctgacttctcttcttgac 1384
Oy 1561 TCTGTTCATGTTCAATTCATGCTGCTGCTACTTGTATGACAGACACTTCTTAATGAATGC 1620
Db 1385 tctgttctcagtttcaatctcagctgctgacttgaagacagactctctaaatgagtg 1444
Oy 1621 AATTTGATACATATGTAATATGACATGCTGCTTCTTCTGAGATGAATTTACAGTGC 1680
Db 1445 aaattgataaataatgtaataatgacactcagtttcttgcagataaacttcaacgctc 1504
Oy 1681 TTTCTATACCTGTGAGCTGATACCTCTTATAGAAATTCAAAAGCTTCAGCTTCTTTC 1740
Db 1505 tctgtatacgttgaaggtacactcttataagaagatcaaaagctcagctctcttcttc 1564
Oy 1741 TTTCTACTCCAGTGAATGATGGGCTCTGCTCAAGTTGAAGAGTCTTATTTGACATG 1800
Db 1565 ttcttaactccagtgtaagtaatggtctcctgctcaagtgaagaagttccatcttgcactg 1624
Oy 1801 TAGCCTGCGCTGTGTAATGAGCATCTATTAATCGGCTTCA 1846
Db 1625 tagctcgcgctgctgtaattgagacatcttataatcgcttca 1670

RESULT 7
US-08-340-539A-11
: Sequence 11 Application US/08340539A
: Patent No. 3808025
: GENERAL INFORMATION:
: APPLICANT: Tedder, Thomas F.
: APPLICANT: Kansas, Geoffrey S.
: TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
: TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/340,539A
: FILING DATE: 16-NOV-1994
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/008,459
: FILING DATE: 25-JAN-1993
: ATTORNEY/AGENT INFORMATION:

```

NAME: Gunnison, Jane  
REGISTRATION NUMBER: 38,479  
REFERENCE/DOCKET NUMBER: CG-104 CON  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1696 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-340-539A-11

Query Match 40.8%; Score 922.2; DB 1; Length 1696;  
Best Local Similarity 97.8%; Pred. No. 3.9e-261;  
Matches 989; Conservative 0; Mismatches 13; Indels 9; Gaps 5;  
QY 1227 AGTATGATGACCCATTTAAATCGCCCTGGTGAAGAAATTCCTGGAACTAAATAA 1286  
DB 308 AGTATGAAAGACCCATTTAAATCGCCCTGGTGAAGAAATTCCTGGAACTAAATAA 367  
QY 1287 TCATGATGATCCTTTAAATCGCCCTGGTGAAGAAATTCCTGGAACTAAATAA 1346  
DB 368 TCATGATGATCCTTTAAATCGCCCTGGTGAAGAAATTCCTGGAACTAAATAA 427  
QY 1347 ACATGAAGTGTG-TTCCTTCAGTGCATCTGGGAAGATTTCTACCCGACACAGTTCCT 1405  
DB 428 ACATGAAGTGTGTCCTTCAGTGCATCTGGGAAGATTTCTACCCGACACAGTTCCT 487  
QY 1406 CAGCTTCATTTGCGCCCTCATTTATCCCTCAACCCCGACCCAGAGTGTTTATACAGC 1465  
DB 488 CAGCTTCATTTGCGCCCTCATTTATCCCTCAACCCCGACCCAGAGTGTTTATACAGC 547  
QY 1466 TCACGTTTTGCTTTTCGAGGAAGAAATTAAGACCAT-AAAGGAAAGAGTTCATGT 1524  
DB 548 TCACGTTTTGCTTTTCGAGGAAGAAATTAAGACCAT-AAAGGAAAGAGTTCATGT 607  
QY 1525 GGAATATAAAGATGCTGACTTGTCTCTTTCTTGAATCTGTTTTCAGTTCAATTCAGT 1584  
DB 608 GGAATATAAAGATGCTGACTTGTCTCTTTCTTGAATCTGTTTTCAGTTCAATTCAGT 667  
QY 1585 GCTGACTGATGACAGACATCTTAAATGAAGTGAATTTGATACATATGTAATATG 1644  
DB 668 GCTGACTGATGACAGACATCTTAAATGAAGTGAATTTGATACATATGTAATATG 727  
QY 1645 GACTCAGTTTTCTGACAGATCAATTTACAGTCTTCTGTAATACGTGGAGGTACAT 1704  
DB 728 GACTCAGTTTTCTGACAGATCAATTTACAGTCTTCTGTAATACGTGGAGGTACAT 786  
QY 1705 CTATTAAAGACTCAAAAGTCTAGCTCTCTTTCTTAACTCCAGTGAATATG 1764  
DB 787 CT-----ATGAAGTCAAAAGCTACGCTCTCTCTTTCTTAACTCCAGTGAATATG 841  
QY 1765 GGTCTGCTCAAGTTGAAGAGTCTTGTGACTGAGCTGCGCTCTGTGAATTTGA 1824  
DB 842 GGTCTGCTCAAGTTGAAGAGTCTTGTGACTGAGCTGCGCTCTGTGAATTTGA 901  
QY 1825 CCATCTATTAACTGCTTCAGGCTCCCGACCTTCTTACGACCTCTCTTTTCAGT 1884  
DB 902 CCATCTATTAACTGCTTCAGGCTCCCGACCTTCTTACGACCTCTCTTTTCAGT 960  
QY 1885 TGCTGACTTCACACCTACATCTATGAGTCCCAAGCAAAAGAGAGAGAGAAAT 1944  
DB 961 TGCTGACTTCACACCTACATCTATGAGTCCCAAGCAAAAGAGAGAGAGAAAT 1020  
QY 1945 AGCTGAGGCGTTTTAGTTGGGGTTTTGCTTTCTTTTATGAAACCATTCCTA 2004  
DB 1021 AGCTGAGGCGTTTTAGTTGGGGTTTTGCTTTCTTTTATGAAACCATTCCTA 1080  
QY 2005 TTCTTATAGTCAATGTTCTCTTTTATCAGATATATATGTAAGAAACATCATCTAAT 2064

DB 1081 TTCTTATAGTCAATGTTCTCTTTTATCAGATATATATGTAAGAAACATCATCTAAT 1140  
QY 2065 GCTAGCTCAAGTACATCTCTTGTATGTCATATGGAAGATTTAAACAGGTGAGAAAT 2124  
DB 1141 GCTAGCTCAAGTACATCTCTTGTATGTCATATGGAAGATTTAAACAGGTGAGAAAT 1200  
QY 2125 TCCTTGATTCACATGAATGCTCTCTTTCCCTGCGCCGAGACCTTTATCGACTTAC 2184  
DB 1201 TCCTTGATTCACATGAATGCTCTCTTTCCCTGCGCCGAGACCTTTATCGACTTAC 1260  
QY 2185 CTAGATCTACATATATCTTTAAATTTATCATGACAGCCTCCCTCAACCCAC 2235  
DB 1261 CTAGATCTACATATATCTTTAAATTTATCATGACAGCCTCCCTCAACCCAC 1311

RESULT 8  
US-08-461-592B-11  
Sequence 11, Application US/08461592B  
Patent No. 5834425  
GENERAL INFORMATION:  
APPLICANT: Fedder, Thomas F.  
APPLICANT: Kansas, Geoffrey S.  
TITLE OF INVENTION: CHIMERIC SELECTINS AS STIMULANEOUS  
TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Weingarten, Schurglin, Gagnebin & Hayes  
STREET: Ten Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,592B  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/340,539  
FILING DATE: 16-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/008,459  
FILING DATE: 25-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: CG-104  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1696 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-461-592B-11

Query Match 40.8%; Score 922.2; DB 2; Length 1696;  
Best Local Similarity 97.8%; Pred. No. 3.9e-261;  
Matches 989; Conservative 0; Mismatches 13; Indels 9; Gaps 5;  
QY 1227 AGTATGATGACCCATTTAAATCGCCCTGGTGAAGAAATTCCTGGAACTAAATAA 1286

[illegible]

RESULT 9  
US-08-513-278-3  
; Sequence 3, Application US/08513278  
; Patent No. 5840844  
; GENERAL INFORMATION:

```

1 APPLICANT: LASKY, LAURENCE A.
2 APPLICANT: STACHELL, SCOTT E.
3 APPLICANT: ROSEN, STEVEN D.
4 APPLICANT: SINGER, MARK S.
5 APPLICANT: YEDNOCK, TED A.
6 TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
7 NUMBER OF SEQUENCES: 6
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Genentech, Inc.
10 STREET: 460 Point San Bruno Blvd
11 CITY: South San Francisco
12 STATE: California
13 COUNTRY: USA
14 ZIP: 94080
15
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: patin (Genentech)
21
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/513, 278
24 FILING DATE: 10-AUG-1995
25 CLASSIFICATION: 5530
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 08/059027
28 FILING DATE: 06-MAY-1993
29 APPLICATION NUMBER: 07/786149
30 FILING DATE: 31-OCT-1991
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 07/315015
33 FILING DATE: 23-FEB-1989
34 ATTORNEY/AGENT INFORMATION:
35 NAME: Dreger, Ginger R.
36 REGISTRATION NUMBER: 33, 055
37 REFERENCE/DOCKET NUMBER: 565D1C1
38 TELECOMMUNICATION INFORMATION:
39 TELEPHONE: 415/225-3216
40 TELEFAX: 415/952-9881
41
42 TELEX: 910/371-7168
43 INFORMATION FOR SEQ ID NO: 3:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 2214 bases
46 TYPE: nucleic acid
47 STRANDEDNESS: single
48 TOPOLOGY: linear
49
50 US-08-513-278-3

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Query	Match	Similarity	Score	DB	Length
Best Local	Similarity	73.4%	Pred.	7.3e-242	
Matches	1160	Conservative	0	Mismatches	392
				Indels	28
				Gaps	4
Qy	92	GGGCTGCAGAAAGTGAAGGACCAAGCAAGCATGATATTTCCATGGAAATGTCA	151		
Db	69	GGCTGCAGAGACTTGCAGAGAGAGCCAGCAAGCATGCTTTCCATGGAGATGTA	128		
Qy	152	GAGCACCCGAGAGACTTATGGAACTCTTCAAGTTGTGGGGGTGCAANTCCTGTGG	211		
Db	129	GGGTACTTACTGGGGCTCGAGGAACTCTGAAGTGCTGGGTGTGGACACTGCTGTGG	188		
Qy	212	TGATTTCCCTGCACATCATGGAACCTACTGCTGGACTTACCATTTATTCGAAAACCCAT	271		
Db	189	TCACCTTCGATATACCATGGAACCTCACTGTTGGACTTCCATTTATTCGAAAAGCCCAT	248		
Qy	272	GAACTGGCAAGAGGCTAGAAAGATTCCTGCCGAGACATTCACAGATTTGTGGCCATTA	331		
Db	249	GAACTGGCAAAATGCTAGAAAGCTTCGCAAGCAAAATTAACAGATTTAGTGCCTATTA	308		
Qy	332	AAACAGGGGAAATGATATCTGGAGAAAGCTCGCCCTTCAGTCGTTCTTACTAGT	391		
Db	309	AAACAGAGAGAAATGATATTTAGAGAAATACATTGGCCCAAAAGCCCTATTACTAGT	368		
Qy	392	GATAGGAATCCGGAAGATAGGAGAAATATGACGTCGGTGGGAACCAACAATCTCTCAC	451		

Db	1447	AGAGTATTTTTATCACTTTTCTGTGGAGAAC-----AAGCAAAAGTGTACTGT	1497
QY	1525	GAAGATTAAGATGAGCTACTTTGGCTGTTCTGACTCTGTTTTCAGTTTTCAGTAATGAGT	1584
Db	1498	AGAAATTAAGACAGCTGTTTACTCTTTCCTCAACCTGTTTCTTCTAGTAAATTCAC	1557
QY	1585	GCCTGCTCTGATGACAGCACTTCTTAATGAGTGCAATTTGATACATATGTGAATATG	1644
Db	1558	ACGAAGCTTAATGCAAAACAC-----AGTGAATAATGATCCATGACTAATTTGGA	1607
QY	1645	GACTAGTTTCTTTCAGAGAT	1664
Db	1608	AACTAGACTCCTTTCGCAT	1627
RESULT	10		
	5514582-3		
	: Patent No. 5514582		
	: APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.		
	: TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID		
	: IMMUNOGLUBULINS		
	: NUMBER OF SEQUENCES: 43		
	: CURRENT APPLICATION DATA:		
	: APPLICATION NUMBER: US/08/185,670		
	: FILING DATE: 21-JAN-1994		
	: PRIOR APPLICATION DATA:		
	: APPLICATION NUMBER: 986, 931		
	: FILING DATE: 08-DEC-1992		
	: APPLICATION NUMBER: 808,122		
	: FILING DATE: 16-DEC-1991		
	: APPLICATION NUMBER: 440,625		
	: FILING DATE: 22-NOV-1989		
	: APPLICATION NUMBER: 315,015		
	: FILING DATE: 23-FEB-1989		
	: SEQ ID NO.3:		
	: LENGTH: 2214		
	5514582-3		
Query Match	37.9%	Score 856.8:	DB: 5:
Best Local Similarity	73.48%	Pred. No. 7,3e-242:	Length 2214:
Matches 1160:	Conservative 0:	Mismatches 392:	Indels 28:
		Gaps	4
QY	92	GGGCTGCAGAGAAGAACTAGAGAGAGACCAAGCAAGCAATGATATTTCCATGGAATGTCA	151
Db	69	ggctcgagagagagcttcgagagagagccagcaagcatggttccatgagatgta	128
QY	152	GAGCAAGCCAGAGGGCACTTATGAGAACTTCTCAAGTTGTTGGGGGTGGACATGCTCTGTTG	211
Db	129	gggtactactgagggcctcgaggaacatctctgaagctggtggtcgaactgctctgtg	188
QY	212	TGATTTCTTGACACATCATGAGACCTACACTGCTGAGCTTACCATTAATTCGAAAAACCAT	271
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QY	272	GAACTGGCAAGGGCTTGAAGAATTCTGCCGAGACAAATTACACAGATTTAGTTGCCATACA	331
Db	249	gaactggaaaatcgtcagaagaattctgcgaagaaaattacacagatttagtgcataca	308
QY	332	AAACAAAGCCGAATTTAGATCTGGAAGAGACTGTGCCCTTTCAGTGGCTTCATACATCG	391
Db	309	aaacaagaagagaatctgagatatttgaataatacatctgcccacaagaagccattactactg	368
QY	392	GATAGCAATCCGAGAGATAGAGGAATATGACGTTGGCTGGCAACAAACAATCTCTCAC	451
Db	369	gataagatcagaagaatttggaaaatltgacatlggttgggaaccacaacaactctcac	428
QY	452	TGAAGAAAGCAAAATGTTGGGAGATGTGTGAGCCCAACAAACAAGAAACAAGAGAGACTG	511
Db	429	taaaagacgagaaactcgtgggtgcgcgtgggagccacaacaagaagatcccaaggaagactg	488
QY	512	CGTGGAGCTTATATCAAGAGAAACAAGATGACAGCAATGGAAGATACACCTTGCCA	571

Dh	489	tggagagatctataatacaagaggagaagaagactctcgggaaatagaaagatgaagccctgta	548
Qy	572	CAAACTAAAGCGACCCCTCTGTACACAGCTCTTGGCCAGCCCTGGTCATGACGTGGCCA	631
Dh	549	caaaagaaagcagctctctctctacacagcctcttcgcagccagggctcttgcgaatggccg	608
Qy	632	TGGGAATGTGTACAAATTCATCATAATTCACACTGCAACTGTGTATGTGGGTGACTATG	691
Dh	609	tggagaaatgtgtggaataactcaacaataacacgtgcatctgtgaatgcaaggtatatacgg	668
Qy	692	GCCCCAGTGTACGCTTGTGATCTTTCAGTGTGAGCCCTTTCGAGCCCCGACAGCTGGGTACAT	751
Dh	669	gccccagtgtaagataatgtgtccaggttgagaccttggaagggcccccagatcttgagtaact	728
Qy	752	GGACTGTACTCACCCTTTGGAAACTTCAGCCTTCAGCTCACAAGTGTGCTTTCAGCTGTC	811
Dh	729	ggactgtactccaccctctggaaacttcagcttccagttccagttcgaatgtgcttcaactctgc	788
Qy	812	TGAAGAACAACTTAATCTGGGATTTGAAGAACACCTGTGGACATTTTGGAACTGGTC	871
Dh	789	tgaaggaaagagactactcttggaacttcagaaacaacagttggaagcatcttgaaactgctc	848
Qy	872	ATTCACGAACAACCTGTCAAGTGATTTTCAGTGTGACCCCTTCATCAGCACCAATTTGG	931
Dh	849	atctcccaagccaactctgcacaagtcgaccagtggaagctcttggaagggcccccgaatctgg	908
Qy	932	GATCATGACGTGTGCCCATCCCTGGCCAGCTTCAGCTTTCACCTGTGCATGTACCTTTCAT	991
Dh	909	taccatgtgactgcataccaccctctggaaacttcagttccagttccaaagtgtcttcaa	968
Qy	992	CTGCTCAGAGAGAACTGACTTAATTTGGGAAGAAACCAATTTGTGATCATCTGGAAT	105
Dh	969	ctgtctctgaggaagagagactactcttggaacttcgaaacaacagttggaagcatctgga	1022
Qy	1052	CTGGCTAAATCTCTGTCAATATATCTCAAAATTTGCAGAAAGTTTCATCAATGTTAA	1111
Dh	1029	ctgtgtcatctccagagccaactctgcacaagagacaacaagaatcttccaaagatccaaga	108
Qy	1112	GGCTGATTAATTAACCCCTCTTCATTTCCAGTGGCAGTCAATGTTACAGATTTCTGTGGT	117
Dh	1089	agggtgactacaaccctctctcatctctctgtgacggtcatgtgtccagcactctccgggct	1144
Qy	1172	GGCATTTATCTTTGGCTGGCAGAGAGATTAAAAAGCCAGAAATCCAGAGAGAT	123
Dh	1149	ggcatctctcatcttggctctggcagggcggttaaaaaaggaagaactctcaagaagaagat	120
Qy	1232	GAATGACCCATATTAAATTCGCCCTTGGTGGAAAGAAATTTCTG-----GAATACTAA	128
Dh	1209	ggaatgactcaactaactgactatcatcctcttgaaaggaagccaagaatgcttaagaacaaa	126
Qy	1285	AATCATGAGATCTTTAAATCTTTCATGCAAAAGTTTGTGTGGACACTGCTCACTGTC	134
Dh	1269	catgtgaaataaagaatcaagtctccctcgtaagaattttaaagcgagcatcttcccaat	132
Qy	1345	AAACATGAAGTGTGTTCTTCACTGATCTGTGGAGATTTCTACCCGACCAACAGTTTCT	140
Dh	1329	agagaatcgagtggttcg--tcaacgaactcggagaagattcttcatcgaaccaagctcct	138
Qy	1405	TCGACTTTCATTTGGCCCCCATTTATCCCTCAACCCCGACCCACAGGTGTTTATACAG	146
Dh	1387	ctcaatctcccttcgctcatctcatcccaataaccctatcccaataatgltgtatatacag	144
Qy	1465	CTCAGCTTTTGTGTTTTCGTGAGAGAAACAAATTAAGACCATTAAGGAAAGGTTATGCT	152
Dh	1447	agtgatattatcatcatcttctcgttggaagac-----aagcaaaagtctacgct	149
Qy	1525	GAATATTAAAGATGGCTGACTTGTGCTTTCTTGAAGCTGTGTTTTCAGTTTCATTAACAT	158
Dh	1498	agaataaagaacagcgcttcttaactcttccctaactctgttctcgtatgtaactcagc	155
Qy	1585	CGTGTACTTGTATGACAGACACTTCTTAATATCAAGTGCMAATTTGATACATATGTGAATATG	164
Dh	1558	acagaagcctaataatgcaaaaac-----agtgaataatatacatcagaatgaaatctgga	160

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QY 1645 GACTGAGTTTCTGTGCAGAT 1664
Db 1608 aactcagactccttgcgcac 1627

RESULT 11
US-08-340-539A-5
; Sequence 5, Application US/08340539A
; Patent No. 5808025
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340.539A
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gunnison, Jane
; REGISTRATION NUMBER: 38,479
; REFERENCE/DOCKET NUMBER: CG-104 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-340-539A-5

Query Match 17.1%; Score 385.2; DB 1; Length 531;
Best Local Similarity 99.2%; Pred. No. 1.2e-103;
Matches 387; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 213 GATTTCCTGCGCAGCATCATCGAACCTCACTGCTGCGACTTACCATTTATTCGAAAAACCCATG 272
Db 72 GATTTCCTGCGCAGCATCATCGAACCTCACTGCTGCGACTTACCATTTATTCGAAAAACCCATG 131

QY 273 AACTGGCAAAAGGGCTAGAGAATTCTGCGCGAGACATTTACACAGATTTAGTTCGCATTACAA 332
Db 132 AACTGGCAAAAGGGCTAGAGAATTCTGCGCGAGACATTTACACAGATTTAGTTCGCATTACAA 191

QY 333 AACCAAGCGGGAATTTGACTATCTGGAGAGAAGACTCTGCCCTTCAGTTCGTTCTTACTACTGG 392
Db 192 AACCAAGCGGGAATTTGACTATCTGGAGAGAAGACTCTGCCCTTCAGTTCGTTCTTACTACTGG 251

QY 393 ATAGCAATTCGGAACATACAGAGATATTCGAGCTGGGTGGGAGAACCAACAATCTCTCACT 452
Db 252 ATAGCAATTCGGAACATACAGAGATATTCGAGCTGGGTGGGAGAACCAACAATCTCTCACT 311

QY 453 GAAAGAGAGAGAAATCTGGGGAGATGTGAGCCCAACAAGAAAGAAACGAGGAGACTGC 512

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Db 132 AACTGSCAAAGGCGCTAGACAGTCTTCCAGACAAATTACACAGATTAGTTGCCATACAA 19

Oy 333 AACCAAGCGGAATTGATGATCTGGGAAGACCTGCGCCCTCACTGTTTACTACTGG 39

Db 192 AACCAAGCGGGAATTGAGTATCTGGGAAGACCTGCTGCTTCACTGCTTCTTACTACTGG 25

Oy 393 ATAGCAATCCGGAAGTAGGAGGAATATGACGTGGGTGGGAACCAAAATCTCTCACT 45

QY 453

Db 312 GAAGAGCAGAGAACTGGGAGATGG

QY 513 GTGAGATCTATATCAAGGAAGAAACAAACATCCAGGCAATGGAAACATGACCCGCGCAC 577  
 |||||  
 Db 372 GTGAGATCTATATCAAGGAAGAAACAAACATCCAGGCAATGGAAACATGACCCGCGCAC 431  
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 QY 573 AAACCTAAGGCAAGCCCTCTGTTACCAAGCT 602  
 |||||

RESULT 13  
US-08-365-470-2

Patent No.5632991  
GENERAL INFORMATION:  
APPLICANT: Gimprone, Jr., Michael A.  
TITLE OF INVENTION: Antibodies Specific For E-selectin And The Use  
THEREOF  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:

STREET: 1100 New York Ave., NW  
CITY: Washington  
STATE: DC

COUNTRY: USA  
ZIP: 20005

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPTON: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Raptor 1.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/365 470

PRIOR APPLICATION: 424  
CLASSIFICATION: herewith  
FILING DATE:

APPLICATION NUMBER: US 08/102,510  
FILING DATE: 05-AUG-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/850,802  
FILING DATE:

FILED DATE: 13-MAR-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Markovitz, Kenneth

REGISTRATION NUMBER: 36,351  
REFERENCE/DOCKET NUMBER: 0627 135

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2600

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS.

LENGTH: 1833 base pairs  
TYPE: nucleic acid  
CDNA: yes

HANDNESS: single  
 TOPOLOGY: linear  
 FEATURE:

NAME/KEY:	nucleic acid
LOCATION:	1-1833

LOCATION: 1-1833  
OTHER INFORMATION: / label = nucle  
OTHER INFORMATION:

OTHER INFORMATION: / label = nucle  
/note = SEQ ID



OTHER INFORMATION: base pair position 1949.  
US-08-365-470-2

Query Match 13.7%: Score 310; DB 1: Length 1833;  
Best Local Similarity 60.6%: Pred. No. 2.8e-81;  
Matches 508; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

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QY 242 CTGACCTTACCAATTTATCTGAAAAACCCATGCMCTGCAAAAGGCTAGAAATCTGCCG 301
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Db 63 CTGGCTTACAAACACCTCCAGGAAAGCTATGACTATGATGAGCGCAGTGTATTTGCA 122
QY 302 AGACAATTACACAGATTTAGTTCATACAAAACAGCGGAAATTTAGTATCTGAGAA 361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 GCAAAAGTACACACACCTGTTGCAATTCAAAACAAAGAGATTTGATACCTTAACCTC 182
QY 362 GACTCTGCCCTTCACTGCTTCTACTAGTATGGAATCCGGAAGATATGAGGATATG 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 183 CATATTGAGCTATTCACCAAGCTTATCTGATTCGAATTCAGAAAAGTCAACAATGTGTG 242
QY 422 GACGTGGGTGGGACCAACAAATCTCTCATGAAAGCAGAGACTGGGAGATGTGA 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 243 GGTCTGGGTAGAACCCAGAAAACCTCTGACAGAAAGAACCAAGAACTGGCTCCAGGTGA 302
QY 482 GCCCAACACAAAGAAGAACAGAGACTCGCTGGAGATCTATATCAAGAGAACAAAGA 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 303 ACCCAACAATAGGCAAAAAGATGAGACTGCGTGGAGATCTCATCAAGAGAAAAGA 362
QY 542 TGCAGGCAATGGAACGATGACGCTGCGCACAACTAAAGGAGCGCTCTGTACAGAG 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 363 TGTGGGCAATGTGGAATGAGAGGTGAGAGAGCAAGAAAGCTTCCCATATGCTACAGAG 422
QY 602 TTCTTGCCAGCCCTGTATGATGAGAGTGTGAAATGTAATCATCAATATCA 661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 423 TGCCGTGACCAATACATCTCTGACAGTGGCCAGGTATGTGTAGAGACATCAATATTA 482
QY 662 CACCTGCAACTGTGATGTGGGTACTATAGGCCCCAGTGTCACTTGTATTCAGTGTGA 721
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 483 CACTTGCAAGTGTGACCTGGCTTCACTGAGTCAAGTGTGCAAAATTTGTAACCTGAC 542
QY 722 GCTTTGGAAGGCCAGAGCTGGGTACATGAGTACTCTACCCCTTTGGAACCTGAG 781
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 543 AGCCCTTGGAATCCCTGAGCATGGAAGCTGTGTCAGTCAACCACCTGGGAAACTTCAG 602
QY 782 CTTCAGCTCACAGTGTGCTGCTGCTGAGAGAACAACTTAACCTGGATGGAAGA 841
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 603 CTACAAATCTTCTGCTCTATATCAGTGTGATAGGGGTTACTGCCACAGCAGATGAGAGC 662
QY 842 AACCACTGTGAGACCAATTTGGAACCTGTCACTTCAGAACCAACCTGTCAAGTATCA 901
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 663 CATGCAATGTATGTCCTCTGAGGATGAGATGCTCTATTTCCAGCTCCATATGTGTGGA 722
QY 902 GTGTGAGCTCTATACAGACCAAGATTGGGATCATGAACTGTACCATCCCTGGCCAG 961
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Db 723 GTGTGATGCTGTGCAAAATTCAGCCCAATGGTCTGTGAAATGTTTCCAAAACCCCTGGAG 782
QY 962 CTTCAGCTTACCTGCTGATGATCTCATGCTGCAAGAGAACTGATTAATTTGGA 1021
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 783 CTTCACATGAGAACACAACTGTACTTTGACTGTGAAAGAGATTTGACTAATGAGAGC 842
QY 1022 GAAGAAAACCAATTTGTGAATCATGTGAATCTGTCAATCTTACTGCAATATGTCAA 1079
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Db 843 CCAGAGCTTCAAGTGTACCTCATCTGGGAATTTGGGACAAAGCAAGCAAGCTGTAA 900
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RESULT 14  
US-09-209-668-18  
Sequence 18, Application us/09209668A  
Patent No. 6114517  
GENERAL INFORMATION:  
APPLICANT: Monia, Brett P.  
APPLICANT: Xu, Xiaoxing S.  
TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR

TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES  
FILE REFERENCE: ISPH-0336  
CURRENT APPLICATION NUMBER: US/09/209,668A  
CURRENT FILING DATE: 1998-12-10  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 18  
LENGTH: 3834  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (117)..(1949)  
PUBLICATION INFORMATION:  
DATABASE ACCESSION NUMBER: M24736/Jenbank  
DATABASE ENTRY DATE: 1994-11-07  
US-09-209-668-18

Query Match 13.7%: Score 310; DB 3: Length 3834;  
Best Local Similarity 60.6%: Pred. No. 4.1e-81;  
Matches 508; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

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Db 239 gcaaaagtagcacacaccctggttgcaatttcaaaaagaagaagattgtagtaccatctc 298
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Db 419 tgttggtgcatgtagaattgtagaaggtgcaagaagaagaagcttgccatgctacacagc 538
QY 602 TTCTTGCCAGCCCTGTATGATGAGAGTGTGAAATGTAATCATCAATATCA 661
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Db 719 ctacaattcttcctgctctatcagctgtagataggggttaccctgcgaagcagtagggagc 778
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Db 779 catgagtgatgctctctctgtagaagtggtctctctatccagactgcgaatgltgtga 838
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Db 839 gtgtgagctgtgacaataatccagcaatggtctgtggaatgttctcaaaaacccctggaag 898
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RESULT 15  
 US-08-365-470-1  
 : Sequence 1, Application US/08365470  
 : Patent No. 5632991  
 : GENERAL INFORMATION:  
 : APPLICANT: Gimdrone, Jr., Michael A.  
 : TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses  
 : THEREOF  
 : NUMBER OF SEQUENCES: 3  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
 : STREET: 1100 New York Ave., NW  
 : CITY: Washington  
 : STATE: DC  
 : COUNTRY: USA  
 : ZIP: 20005  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/365,470  
 : FILING DATE: herewith  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/102,510  
 : FILING DATE: 05-AUG-1993  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/850,802  
 : FILING DATE: 13-MAR-1992  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Markowicz, Karen R.  
 : REGISTRATION NUMBER: 36,351  
 : REFERENCE/DOCKET NUMBER: 0627.1350003  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 202-371-2600  
 : TELEFAX: 202-371-2540  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 3854 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : US-08-365-470-1

Query Match 13.7%; Score 310; DB 1; Length 3854;  
 Best Local Similarity 60.6%; Pred. No. 4,1e-81;  
 Matches 508; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

QY 242 CTGACCTTACCATATTTCTGAAAAACCATGACCTGCAAAAGGCTTGAAGATTCTGCCG 301  
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 QY 422 GAGTGGGTGGGAACCAAAATCTCTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 481  
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QY 482 GCCCAACAAGAAAGAACAGAGAGACTGCGTGAGATCTATATCAAGAAACAAGA 541  
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Search completed: January 12, 2001, 21:40:23  
 Job time: 18969 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2001, 20:32:12 : Search time 2169.06 Seconds  
(Without alignments)  
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Title: US-09-119-209-1

Perfect score: 2259  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 12197726 seqs, 1773875003 residues

Total number of hits satisfying chosen parameters: 24395452

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

#### SUMMARIES

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1	2259	100.0	2259	15 US-09-119-209-1	Sequence 1, App1
2	2161	95.7	2354	14 US-09-023-655-1154	Sequence 1154, Ap
3	2151.6	95.2	2385	49 US-60-243-521-8	Sequence 8, App1
4	2150	95.2	2385	46 US-60-213-360-1118	Sequence 1118, Ap
5	2150	95.2	2384	17 US-09-396-970-8480	Sequence 8480, Ap
6	2146.8	95.0	2387	36 US-60-118-318-292	Sequence 292, App
7	2129.6	94.3	2387	42 US-60-172-373-15742	Sequence 15742, A
8	2087.6	92.4	2330	1 PCT-US92-03970-1	Sequence 1, App1
9	2087.6	92.4	2330	1 PCT-US94-00909-1	Sequence 1, App1
10	2087.6	92.4	2330	4 US-08-008-459-1	Sequence 1, App1
11	2087.6	92.4	2330	7 US-08-340-539-1	Sequence 1, App1
12	2087.6	92.4	2330	8 US-08-410-569-1	Sequence 1, App1
13	1605.4	71.1	1788	41 US-60-164-285-5139	Sequence 5139, Ap
14	1605.4	71.1	1788	41 US-60-164-285-5456	Sequence 5456, Ap
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16	959.2	42.5	3238	46 US-60-212-659-230	Sequence 230, App
17	959.2	42.5	3238	46 US-60-230-435-754	Sequence 754, App
18	948.2	42.0	3233	45 US-60-207-315-164	Sequence 164, App
19	922.2	40.8	1696	1 PCT-US92-03970-11	Sequence 11, App1
20	922.2	40.8	1696	4 US-08-008-459-11	Sequence 11, App1
21	922.2	40.8	1696	4 US-08-340-539-11	Sequence 11, App1
22	922.2	40.8	1696	7 US-08-410-569-11	Sequence 11, App1
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26	556.6	24.6	745	17 US-09-396-970-6256	Sequence 5762, Ap
27	475.4	21.0	519	17 US-09-396-970-6256	Sequence 6256, Ap
28	451.2	20.0	505	55 US-09-726-811-2121	Sequence 2121, Ap
29	428.2	19.0	487	17 US-09-359-067-46139	Sequence 46139, A
30	420	18.6	421	19 US-09-528-409-107247	Sequence 107247, A
31	407.6	18.0	431	19 US-09-528-409-113317	Sequence 113317, A
32	405.6	18.0	524	16 US-09-240-371-9103	Sequence 9103, Ap
33	402	17.8	524	23 US-09-652-816-2022	Sequence 2022, Ap
34	401	17.8	435	17 US-09-399-720-6114	Sequence 6114, Ap
35	401	17.8	435	16 US-09-289-768-1303	Sequence 1303, Ap
36	394.4	17.5	492	55 US-09-726-811-1825	Sequence 1825, Ap
37	393.4	17.4	464	17 US-09-359-067-41757	Sequence 41757, A
38	386	17.1	454	55 US-09-726-811-1284	Sequence 1284, Ap
39	385.8	17.1	454	17 US-09-359-067-42317	Sequence 42317, A
40	385.6	17.1	454	19 US-09-528-409-107248	Sequence 107248, A
41	385.2	17.1	531	1 PCT-US92-03970-5	Sequence 107248, A
42	385.2	17.1	531	1 PCT-US94-00909-5	Sequence 5, App1
43	385.2	17.1	531	4 US-08-008-459-5	Sequence 5, App1
44	385.2	17.1	531	7 US-08-340-539-5	Sequence 5, App1
45	385.2	17.1	531	8 US-08-410-569-5	Sequence 5, App1

#### ALIGNMENTS

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RESULT 1
US-09-119-209-1
; Sequence 1, Application US/09119209
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: STACHELL, SCOTT E.
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: SINGER, MARK S.
; APPLICANT: YEDNOCK, TED A.
; TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119, 209
; FILING DATE: 20-Jul-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/513278
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059027
; FILING DATE: 6-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/786149
; FILING DATE: 31-OCT-1991
; APPLICATION DATA:
; APPLICATION NUMBER: 07/315015
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0565D1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SBO ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2259 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-09-119-209-1

Query Match      100.0%; Score 2259; DB 15; Length 2259;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      901  AGTGTGAGCTCTATACAGACCAATTTGGGATCATGAAGTGAAGCACTGAGCCCTGGCCA 960
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Db      901  AGTGTGAGCTCTATACAGACCAATTTGGGATCATGAAGTGAAGCACTGAGCCCTGGCCA 960
QY      961  GCTTCAGCTTACCTGTGACATGCTCAATCTGCTCAAGAGAACTGAGTTAATTGGGA 1020
        |||||||
Db      961  GCTTCAGCTTACCTGTGACATGCTCAATCTGCTCAAGAGAACTGAGTTAATTGGGA 1020
QY      1021  AGAAGAAACCATTTTGAATCATCTGGAACTGTGCAATCTCTAGTCCAAATATGCAAA 1080
        |||||||
Db      1021  AGAAGAAACCATTTTGAATCATCTGGAACTGTGCAATCTCTAGTCCAAATATGCAAA 1080
QY      1081  AATTGCAAAAGTTTCTCAATGATTAAGAGAGGCTATTATTAACCCCTCTTCATTCGAG 1140
        |||||||
Db      1081  AATTGCAAAAGTTTCTCAATGATTAAGAGAGGCTATTATTAACCCCTCTTCATTCGAG 1140
QY      1141  TGGCAGTCATGTTTACTGCTATCTGTGGTTGGCATTTTCAATTTGGCTGGCAAGAGAT 1200
        |||||||
Db      1141  TGGCAGTCATGTTTACTGCTATCTGTGGTTGGCATTTTCAATTTGGCTGGCAAGAGAT 1200
QY      1201  TAAAAAAGGCAAGAAATCAAGAGAGATATGAGCCATATTAATTCGCCCTTGCTG 1260
        |||||||
Db      1201  TAAAAAAGGCAAGAAATCAAGAGAGATATGAGCCATATTAATTCGCCCTTGCTG 1260
QY      1261  AAAGAAATTTCTGGAATCTAAAAATCATAGATCCCTTAAATCTCTTCAATGAACGTT 1320
        |||||||
Db      1261  AAAGAAATTTCTGGAATCTAAAAATCATAGATCCCTTAAATCTCTTCAATGAACGTT 1320
```

Qy	1321	TTGGTGGTGGACCTCTACGTCAAAACATGAAGTGTGTCTCTCAAGTCACATGAGAG	1380
Db	1321	TTGTGTGTGGACCTCTCTACGTCAAAACATGAAGTGTGTCTCTCAAGTCACATGAGAG	1380
Qy	1381	ATTTCATCCCGAACCAACAGTTCCTTCAGCTTCATTTGCCTCCATCTATTAATCCCTCAAC	1440
Db	1381	ATTTCATCCCGAACCAACAGTTCCTTCAGCTTCATTTGCCTCCATCTATTAATCCCTCAAC	1440
Qy	1441	CCCAAGCCACAGGTGTATACAGCTTCAGCTTTGTCTTTCTGAGAGAAACAAATTA	1500
Db	1441	CCCAAGCCACAGGTGTATACAGCTTCAGCTTTGTCTTTCTGAGAGAAACAAATTA	1500
Qy	1501	GACCATTAAGGGAAGGATTCATGTGGAAATAAAGAATGGCTACCTTGTCTTCTTAC	1560
Db	1501	GACCATTAAGGGAAGGATTCATGTGGAAATAAAGAATGGCTACCTTGTCTTCTTAC	1560
Qy	1561	TCTGTCTTTCAGTTCAATTCAATGCTGTACTGTATGACAGACACTTCTTAATGAAGTC	1620
Db	1561	TCTGTCTTTCAGTTCAATTCAATGCTGTACTGTATGACAGACACTTCTTAATGAAGTC	1620
Qy	1621	AAATTTGATACATATTCGCAATATGACATCAGTTTCTGACATCAAAATTTACGTCTC	1680
Db	1621	AAATTTGATACATATTCGCAATATGACATCAGTTTCTGACATCAAAATTTACGTCTC	1680
Qy	1681	TTTGTGTATACGTGGAGTACACTCTTTATTAAGAAAGTCAAAAAGTCAAGCTCTCTCTTC	1740
Db	1681	TTTGTGTATACGTGGAGTACACTCTTTATTAAGAAAGTCAAAAAGTCAAGCTCTCTCTTC	1740
Qy	1741	TTTTTAACTCCAGTGAAGTAAATGGGGTCCGTGCAAGTTGAAAGAGTCCATATTGACATG	1800
Db	1741	TTTTTAACTCCAGTGAAGTAAATGGGGTCCGTGCAAGTTGAAAGAGTCCATATTGACATG	1800
Qy	1801	TAGCCTGCGCCTCTGTCAATTGACACATCCATTTTAACTGCGCTTCAGGCTCCACCTT	1860
Db	1801	TAGCCTGCGCCTCTGTCAATTGACACATCCATTTTAACTGCGCTTCAGGCTCCACCTT	1860
Qy	1861	CTTCAGCACCCTCTTTTCAATGGGCGACTCCACACCTAGACATCTCATGAGTGGCA	1920
Db	1861	CTTCAGCACCCTCTTTTCAATGGGCGACTCCACACCTAGACATCTCATGAGTGGCA	1920
Qy	1921	AGCAAAAGGAGAGAGAGAGAAATAGCCTGCGCGGCTTTTATGTTGGGGGTTTTGCTGT	1980
Db	1921	AGCAAAAGGAGAGAGAGAGAAATAGCCTGCGCGGCTTTTATGTTGGGGGTTTTGCTGT	1980
Qy	1981	TTTCCTTTTATGACACCCATTCCTATTTCTTTAATGTCATATGTTCTTTTATACGATATTA	2040
Db	1981	TTTCCTTTTATGACACCCATTCCTATTTCTTTAATGTCATATGTTCTTTTATACGATATTA	2040
Qy	2041	TTTAGTAAGAAACATCACTGAATAATGCACTGAGTGCATCTCTTGAATGTCATATAGG	2100
Db	2041	TTTAGTAAGAAACATCACTGAATAATGCACTGAGTGCATCTCTTGAATGTCATATAGG	2100
Qy	2101	AAGAGTTAAACAGGTGGAGAAATTTCTTGATATTCACAAATGAANTGCTCTCTTCCCTG	2160
Db	2101	AAGAGTTAAACAGGTGGAGAAATTTCTTGATATTCACAAATGAANTGCTCTCTTCCCTG	2160
Qy	2161	CCCCAGAACTTTTATTCACATTAAGATTCACATATTTCTTAAATTCATCTCAGGC	2220
Db	2161	CCCCAGAACTTTTATTCACATTAAGATTCACATATTTCTTAAATTCATCTCAGGC	2220
Qy	2221	CTTCCCTCAACCCACAGGGGGCGGCACACACATGGAATTC	2259
Db	2221	CTTCCCTCAACCCACAGGGGGCGGCACACACATGGAATTC	2259

RESULT 2  
US-09-023-655-1154  
; Sequence 1154, Application US/09023655  
; GENERAL INFORMATION:  
; APPLICANT: Cucco, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Sellhammer

```

1  TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GEN
2  TITLE OF INVENTION: EXPRESSION
3  NUMBER OF SEQUENCES: 1508
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
6  STREET: 3174 PORTER DRIVE
7  CITY: PALO ALTO
8  STATE: CALIFORNIA
9  COUNTRY: USA
10 ZIP: 94304
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC compatible
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: word perfect 6.1 for Windows/MS-DOS 6.2
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/023,655
18 FILING DATE: HERewith
19 CLASSIFICATION:
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER:
22 FILING DATE:
23 CLASSIFICATION:
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Zeller, Karen J.
26 REGISTRATION NUMBER: 37,071
27 REFERENCE/DOCKET NUMBER: PA-0001 US
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (650) 855-0555
30 TELEFAX: (650) 845-4166
31 INFORMATION FOR SEQ ID NO: 1154:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 2354 base pairs
34 TYPE: nucleic acid
35 STRANDEDNESS: single
36 TOPOLOGY: linear
37 IMMEDIATE SOURCE:
38 LIBRARY: GENBANK
39 CLONE: g187182
40 US-09-023-655-1154

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Query Match	Similarity	95-7%	Score	2161;	DB	14;	Length	2354;
Best Local	Similarity	99.4%;	Pred.	No. 0;				
Matches	2200;	Conservative	0;	Mismatches	10;	Indels	3;	Gaps
OY	25	ACCTGCAGCACAGCACACTCCCTTTGGCAGAGGACCTGAGACCCCTTGCTGTAAGTCAAGAG	84					
Db	12	ACCTGCAGCACAGCACACTCCTTTGGGCAAGGACCTGAGACCCCTTGCTGTAAGTCAAGAG	71					
OY	85	GCTCAATGGGCGTGCAGGAAGAACTAGAGAAGGACCCAAGCAAAAGCCATGATATTTCCATGGA	144					
Db	72	GCTCAATGGGCGTGCAGGAAGAACTAGAGAAGGACCCAAGCAAAAGCCATGATATTTCCATGGA	131					
OY	145	AATGTCAGAGCACCCAGAGGGGACTATGAGAACATTTCAAGTTGGGGGGTGGACAATGC	204					
Db	132	AATGTCAGAGCACCCAGAGGGGACTATGAGAACATTTCAAGTTGGGGGGTGGACAATGC	191					
OY	205	TCTGTTGTAATTTCCCTGGCACATCAATGGAACCTACTGCTGCAATACCAATTAATTCGAAA	264					
Db	192	TCTGTTGTAATTTCCCTGGCACATCAATGGAACCGACTGCTGGCACTTACCATTAATTCGAAA	251					
OY	265	AACCCATGAACTTCGGGAAGGGCTAGAAAGATTTTCGCCGAGACAAATTACACAGATTTAGTTTG	324					
Db	252	AACCCATGAACTTCGGGAAGGGCTAGAAAGATTTTCGCCGAGACAAATTAACAGATTTAGTTTG	311					
OY	335	CCATTCAGAAAGAGGCGGGAATTTGATGATTCCTGGAAGAAACACTCTGCCCTTCAGTCTCTTT	384					
Db	312	CCATTCAGAAAGAGGCGGGAATTTGATGATTCCTGGAAGAAACACTCTGCCCTTCAGTCTCTTT	371					
OY	385	ACTACTGATATGGAATCCGGGAAGATAGGAGCAATATGAGACCTGGGGTGGCAACCAACAAT	444					
Db	372	ACTACTGATATGGAATCCGGGAAGATAGGAGCAATATGAGACCTGGGGTGGCAACCAACAAT	431					

Qy	1523	GGGAAATATAAAGATGGCTGACCTTGGCTCTTTCTTGACTCTGTGTTTCACTTCAATTTCA	1582
Db	1512	GTGCAATATATAAGATGGCTGACCTTGGCTCTTTCTTGACTCTGTGTTTCACTTCAATTTCA	1571
Qy	1583	GGCTGTACTTGGATGACAGACACTTCTTAAATGAAGTGCATATTTGATACATATGTAATA	1642
Db	1572	GTGCTGTACTTGGATGACAGACACTTCTTAAATGAAGTGCATATTTGATACATATGTAATA	1631
Qy	1643	TGGACATAGTTTTCTTGGCAGATCCAAATTTGACGTCGCTTCTGTATATCTGGAGGTACA	1702
Db	1632	TGGACATAGTTTTCTTGGCAGATCCAAATTTGACGTCGCTTCTGTATATCTGGAGGTACA	1691
Qy	1703	CTCTTATGAAAGTTTCAAAAAGTCTAGCCTCTCCCTCTTCTTCACTCCAGTGAAGTAT	1762
Db	1692	CTCCTATGAAAGTTTCAAAAAGTCTAGCCTCTCCCTCTTCTTCACTCCAGTGAAGTAT	1751
Qy	1763	GGGCTCTCTGTCAAGTTGAAAGAGTCTTATTTGACATGAGCCTCGCCGCTGTGTAATTG	1822
Db	1752	GGGCTCTCTGTCAAGTTGAAAGAGTCTTATTTGACATGAGCCTCGCCGCTGTGTAATTG	1811
Qy	1823	GACCATCTATTTTAACTGAGCTTCAAGGCTCTCCCACTCTTCAAGCCACTCTCTTTTCA	1882
Db	1812	GACCATCTATTTTAACTGAGCTTCAAGGCTCTCCCACTCTTCAAGCCACTCTCTTTTCA	1870
Qy	1883	GTTGGCTGACTTCCACACCTTGCATCTCATAGTGGCCAAAGAGAGAAAGAGAGAA	1942
Db	1871	GTTGGCTGACTTCCACACCTTGCATCTCATAGTGGCCAAAGAGAGAGAAAGAGAGAA	1930
Qy	1943	ATAGCCCTGGCGGTTTTTTTAACTTTGGGGGTTTTGCTGTTTCTTTTATGAGACCCATTC	2002
Db	1931	ATAGCCCTGGCGGTTTTTTTAACTTTGGGGGTTTTGCTGTTTCTTTTATGAGACCCATTC	1990
Qy	2003	TATTTCTTATAGTCACATGTTTCTTTTATACAGATATATTATAGTAAGAAAACATCAGTAA	2062
Db	1991	TATTTCTTATAGTCACATGTTTCTTTTATACAGATATATTATAGTAAGAAAACATCAGTAA	2050
Qy	2063	ATGCTAGCTGCAAGTGAACATCTCTTTGATGTCAATATGAAAGTAAACAGGTGAGAA	2122
Db	2051	ATGCTAGCTGCAAGTGAACATCTCTTTGATGTCAATATGAAAGTAAACAGGTGAGAA	2110
Qy	2123	ATTCTTTGATTCACAAATGAATGATCTCTCCCTTCCCTCCGACCAATTTTATCCACTT	2182
Db	2111	ATTCTTTGATTCACAAATGAATGATCTCTCTCTTCCCTCCGACCAATTTTATCCACTT	2170
Qy	2183	ACCTTGAATTCACATATTTCTTTAAATTTGATATGACGCTCCCTCCCAACCCAC	2235
Db	2171	ACCTTGAATTCACATATTTCTTTAAATTTGATATGACGCTCCCTCCCAACCCAC	2223
RESULT 3			
US-60-243-521-8			
; Sequence 8, Application US/60243521			
GENERAL INFORMATION:			
APPLICANT: Hopkins, Christopher M.			
APPLICANT: Peterson, David P.			
APPLICANT: Cocks, Benjamin G.			
APPLICANT: Hawkins, Phillip R.			
TITLE OF INVENTION: GENES REGULATED IN ACTIVATED T CELLS			
FILE REFERENCE: PA-0042 P			
CURRENT APPLICATION NUMBER: US/60/243,521			
NUMBER OF SEQ ID NOS: 116			
SOFTWARE: Perl Program			
SEQ ID NO 8			
LENGTH: 2385			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: misc_feature			
OTHER INFORMATION: Template ID: 331616.2			
US-60-243-521-8			



Db 2131 aatccctgattcaacaatgaatgctctccctccctcccgaccagacttataccact 2190  
QY 2182 TACCTAGATTCTACATATTTCTTAATTTTCATCTCAGGCCCTCCCTCAACCCGAC 2235  
Db 2191 tacttagattcatatattctttaaattcaatcccaaggccctcccaacccac 2244

RESULT 4  
US-60-213-360-1118  
; Sequence 1118, Application US/60213360  
; GENERAL INFORMATION:  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Ial, Preeti  
; APPLICANT: Diep, Dinh  
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using  
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor  
; FILE REFERENCE: GX-0014 P  
; CURRENT APPLICATION NUMBER: US/60/213,360  
; NUMBER OF SEQ ID NOS: 8347  
; SOFTWARE: PERL Program  
; SEQ ID NO 1118  
; LENGTH: 2385  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc-feature  
; OTHER INFORMATION: Incyte ID NO: 331616.2  
US-60-213-360-1118

Query Match 95.2%; Score 2150; DB 46; Length 2385;  
Best Local Similarity 99.4%; Freq. No. 0;  
Matches 2200; Conservative 0; Mismatches 10; Indels 4; Gaps 4;

QY 25 ACCTGACGACAGCACATCCCTTT-GGCAAGGACCTGAGACCCCTGTCATAGTCAGAGA 83  
Db 32 accctgacgacagcacactccctcttggcaaggacacctggaaccttctgctaaagcaaga 91  
QY 84 GGCTCAATGGCTGCGAGAGAATAGAGAGGACCCAAAGCCCAATGATATTTCCATGG 143  
Db 92 ggcctcaatggctgcgagagactagagaagaccaaagccatgataattccatg 151  
QY 144 AATGTCAGACACCCCAAGGAGCTTATGGAACATCTTCAAGTTGTGGGGTGGACAAATG 203  
Db 152 aaatgtcagacaccccaaggagactatggaacatcttcaagtgtggtgggagcaatg 211  
QY 204 CTCTGTTGATTTCTGGACATCATGGAACCTACTGCTGACTACCATTTATTGAA 263  
Db 212 ctctgttgtattctctgycacatcatggaacgcgactggaactaccattatctcgaa 271  
QY 264 AAACCCATGAACCTGGCAAGGCGTAGAAGATTCTGCCGAGACAAATTACAGATTAGTT 323  
Db 272 aaacccatgaacctggcaaaaggctagaagaattctgcccgaacaattacacagatttagt 331  
QY 324 GCCATACAAAAGCGGGAATTGATCTCTGAGAGAGCTGGCCCTTCACTGCTCT 383  
Db 332 gccatacaaaagaagcggaattgtatctctgagagaagactctgaccttcaagtcgtct 391  
QY 384 TACTACTGGATAGGAATCCGGAAGATAGAGAAATGAGACGTGGGTGGAAACCAACAA 443  
Db 392 tactactggataggaatccggaagatagagaaatatgacgtygggtgggaaccacaaga 451  
QY 444 TCTCTCACTAAAGACAGAGACTGGGGAGATGATGAGACCTGGGTGGAAACCAACAA 503  
Db 452 tctcttactgaagaagaagaaactggtgagatggtgagcccaacaagaagaagaaga 511  
QY 504 GAGGACTGCGTGGAGATCTATATCAAGAGAAACAAGATGACAGCAAAATGGAACGTGAC 563  
Db 512 gaggactgctgtagatctatatcaagagaacaagaatgacgagcaaatggaacgtgac 571  
QY 564 GCCTGCACAAACTAAAGGACCCCTCTGTTCACACAGCTTCTTGGCCAGCCCTGATCATG 623

Db 572 gccctccacaactaaaggccctctgttaccagaagttcttgccagccctgtatgc 631  
QY 624 AGGCGCATGAGAGATGTTGATAGAAATTCATTAATATCATACACTTCCAACTGTGATGGG 683  
Db 632 agtggccatgagagaatgtgtgaataatcaataatcaactgcaactgtagatggg 691  
QY 684 TACTATGGGCCCACTGTACGCTTGTGATTCAGTGTGAGGCTTGGAGGCCCAAGACTG 743  
Db 692 tactatggccccagtgctcagttgtgattcatgagtgtgaccttggagccccagagctg 751  
QY 744 GSTACCATGAGATGTAATCACCCTTTGGAAACTTCAAGCTTCAAGCTTCAAGTGTGCTTC 803  
Db 752 gtlacacatggaacttaccaccccttggaaacttcaactgcttcaagcttcaagctgcttc 811  
QY 804 AGCTGCTCTGAAGACAAACTTAAGCTGGGTTGGAACAAACCACTGTGACCATTTGGA 863  
Db 812 agctgctctgagaagaacaacttaactcggagatggaagaacaacccctgtagacatttga 871  
QY 864 AACTGTCATCTCCAGAACCAACCTGTCAAGTATTCAGTGTGAGGCTGTATCAGACCA 923  
Db 872 aactgtcatctccagaaacaacctgcaagtgattcaagtgtgagctctatcagacca 931  
QY 924 GATTGGGATCATGAACCTGTAGCATCCCTGCGCCAGCTTACGCTTTACCTGTGATGT 983  
Db 932 gattgggatcatgaacctgtgacatcccttggccaggttcaagcttacccttgcattgt 991  
QY 984 ACCTTCATCTGCTCAGAGAACTGATTAATTTGGGAAGAAACAACTTTGTGATCA 1043  
Db 992 acccttaccctgcacagaagaaactgtaatttgggaagaagaacaacatttgttaaca 1051  
QY 1044 TCTGGAATCTGTCGAATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1103  
Db 1052 tctggaaatctggtcaaatcccttgaataatgtaataatgtaataatgtaataatgtaata 1111  
QY 1104 ATTAAGAGGGGTGATTATTAATCCCTCTTCAATTCAGTGTGAGGCTGTATTCATGATTC 1163  
Db 1112 attaaagagggtgattataaaccctcttcaatcccttcaatcccttcaatcccttcaatcc 1171  
QY 1164 TCTGGGTTGGCATTTATCATTTTGGCTGGCAAGAGATTAATAAAGGCAAGAAATCCAA 1223  
Db 1172 tctggggttggcatattatcatcttgccttgcaggaagatataaagaagaagaatccaa 1231  
QY 1224 AGAAGTATGAATGACCCATTAATTAATCGCCCTTGGTGAAGAAATTTGTGATTAATTA 1283  
Db 1232 agaagatgaatgaacccatataataatcccttgccttgcaggaagatataaagaagaat 1291  
QY 1284 AATTCATGAGATCTTAAATCTTTCATGAAACGTTTGTGTGTGACACTCTCACTG 1343  
Db 1292 aatcatgagatccttataatccttccatgaaagcttltgtgtgtgtgtgtgtgtgtgt 1351  
QY 1344 CAACATGAGAGTGTG-TTCCTTCAAGTGCATGCGGAGAGATTTTCAACCCAGCAACAGTTC 1402  
Db 1352 caaacatgagagtggttcttcccttccatgcatctggaagatttcttaccctgaccaaag 1411  
QY 1403 CTTCAGCTTCATTTGCGCCCTCAATTTATCCCTCAACCCCGCCAGCTGATTTATAC 1462  
Db 1412 ctctcagcttccatcttgccttccatcttacccttccatcccccagcccaagtgcttacc 1471  
QY 1463 AGCTAGCTTTTGTCTTTTGTGAGAGAAACAATTAAGACAT-AAGGGAAGGATTTGA 1521  
Db 1472 agctagcttcttgtcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1531  
QY 1522 TGTGGAATATTAAGATGCGTGCATTTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1581  
Db 1532 tgtggaatatataaagatgctgcacttgccttcttcttcttcttcttcttcttcttcttct 1591  
QY 1582 AGTGTGACTTGTGAGACAGACACTTCTTAATGAAGTGAACAAATTTGATACATATGTAAT 1641  
Db 1592 agtgtgtacttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1651  
QY 1642 ATGAGACTCAGTTTCTTGGAGATCAATTTCAAGCTGTCTCTGTATTAAGTGTGAGAGTAC 1701



Db	1652	atgagactcagttctctctgcgcagatccaatttcaagtcgctctctctgtatbaetctgtgaggttac	1711
Oy	1702	ACTCTTATAGAAAGTTCAAAAAGCTTACAGCTCTCTCTTTCTTTCTTATACCTCAGTGAAGTAA	1761
Db	1712	actcttatagaagaattcaaaaaagcttaagctctcctctctctcttctcttaactccagtgaaagtaa	1771
Oy	1762	TGGGGTCTCTGCTCAAGTTTGAAAGAGTCCCTATTTTGGCACTGTAGCCTCGCCGTCTGTGAATT	1821
Db	1772	tggggctctctcctaagttcgaagaagtccttaatttcgaactgtgaagctctgcgtctctgtgaatt	1831
Oy	1822	GGACATACCTCTTTTAACTGGCTTCAGAGCCCTCCACACCTTCCTTACAGCACTCTCTTTTTC	1881
Db	1832	ggacatacctaatttaacttgaactgtcctta-gcctcccaacctctctctcaagccactctctcttttc	1890
Oy	1882	AGTTGGCTGACCTTCCACACCTTAGCATCTCATGAGTGCACGAAGCAAAAGAGACAGAGAGA	1941
Db	1891	agttggctgacttccacacacttagcatctcatatgagtgccaagaanaagtgagaagaaga	1950
Oy	1942	AATAGCTCGCGGGTTTTTTAGTTTGGGGTTTTTGCTGTTTCTTTTATGAGACCATTC	2001
Db	1951	aatagcctgcgcgtcttcttttagttctgggggttctgctctgtctctcttaattgagcccaatlc	2010
Oy	2002	CTATTCTTATAGTCATCTGTTCTCTTTATACAGCATATATATAGTAAAGAAACATCATCTGA	2061
Db	2011	ctattcttctaataagcaactgtctctcttcaacaagatactatctgataagaanaaacatcaacga	2070
Oy	2062	AATGCTACGTCGACAGTACATCTCTTTTGATGTCTATGGAAGAGTTTAAACAGTGGAGAGA	2121
Db	2071	aatgctagctgcgaagtgaacatctctcttgatgcataatgagaagatctaaacagctgagaga	2130
Oy	2122	AATTCTTTGATTCACATGTGAATGCTCTCTTTCCCTGCCCCAGAACTTTTATTCACT	2181
Db	2131	aattctcttgattccacaatgaatgcctctctctccctgcgcccgagaacttlatccact	2190
Oy	2182	TACCTAGATTCATATCTCTTTTAAATTCATGTACAGGCTCCGCAACCCAC	2235
Db	2191	tacctagattctacatactctcttcaaatctcaatctcaagcctctccccaacccaac	2244
RESULT 5			
US-09-396-970-8480			
: Sequence 8480, Application US/09396970			
: GENERAL INFORMATION:			
: APPLICANT: Gearling, David P.			
: APPLICANT: Kingsbury, Gillian A.			
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A			
: FILE REFERENCE: MN98-40PA			
: CURRENT APPLICATION NUMBER: US/09/396,970			
: CURRENT FILING DATE: 1999-09-14			
: EARLIER APPLICATION NUMBER: 60/100,293			
: EARLIER FILING DATE: 1999-09-14			
: NUMBER OF SEQ. ID NOS: 8756			
: SOFTWARE: FastSeq for Windows Version 3.0			
: SEQ ID NO 8480			
: LENGTH: 2564			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: misc_feature			
: LOCATION: (1)..(2564)			
: OTHER INFORMATION: n = A,T,C or G			
: US-09-396-970-8480			

	95.28;	Score	2150;	DB	17;	Length	2564;	
	Best Local Similarity	99.48;			Pred. No.	0;		
	Matches 2200:	Conservative	0;		Indels	10;	Gaps	4;
Oy	25 ACCTCAGACAGCGCACACTCCCTTTT-GGCAGAAGACTTGATGCCCTTCGTAAATCAAGA	83						
Dd	50 accgcagcacacgacgaactcccttggcgcaagaacctgagacccttggtctaagtccaaga	109						

QY	84	GGTCATATGGCTGCAGAAAGAACTAGAGAGACCAAGCAAAAGCCATGATATTTCATG	143
Db	110	ggctcaatctggtctgcaagaagaaactagagaagaccgaagaagccaatgatacttccatg	169
QY	144	AAATGTCACAGACCCACAGGGGACCTTATGGAACATCTTTCACCTTGGGGTGGACAATG	203
Db	170	aaatgcacagagacccaagaaggactatggaacaccttcaagctgtaggggtggacaaag	229
QY	204	CTCTGTGTGGATTTTCCCTGGCACATCATGTGAACCTACTGCTGCATCTTACCATTTCTGAA	263
Db	230	ctctgtgtgattcttcctgtgcacatcatggaaccgagctgtgacttaccatcttcgaa	289
QY	264	AAACCCATGACTGGCAAAAGGCGCTGAGAAATTTCTGCCGAGACATTTACACAGATTTAGTT	323
Db	290	aaacccatgaacttggcaaaaggctagaagattctgcggacaattacacagatttagt	349
QY	324	GGCATTAACAACAAGCGGGAATTTAGATTTCTTGAGAGAGACCTCTGCCCTTTCAGTGTCTT	383
Db	350	ggcatatacaaaacaagcggaatactgagatactcggaagaagctctgccttccagtcgctt	409
QY	384	TACTACTGATAGAAATCCGGAAGATAGAGAGAAATATGGACCTGGGTGGGAACCAAAA	443
Db	410	tactactgatagataccggaaagatagaggaatactagaaatggtgtgggaaccacaaa	469
QY	444	TCTCTACTGAGAAAGCAGAGAACTGGGAGATGGTGAGCCCAACACAGAAGAACAG	503
Db	470	tctcttacttgaagaagcagagaagctggggagatggtgagcccaacaagaagaacaag	529
QY	504	GAGGACTGGCTGGACATCTATTTCAGAGAAACAAGATGCGAGCAATTTGAAACCATGAC	563
Db	530	gaggacttggtaggaatctatactcaagaagaacaagaatgcagaaatggaacagtagac	589
QY	564	GCCTCCACAACATTTAAAGCAGCCCTCTGTTCACAGACTTCTTGGCACCCCTGGTCATAC	623
Db	590	gctctgcacaacaactaaaggcagccctctgtctacaagcttcttgcgcagccctggtcagc	649
QY	624	AGTGCCATGAGAAATGTGTAGAAATCATCAATTAATCACACCTGCACTGTGATGTGGG	683
Db	650	agtgcgcataggaatctgttagaaatcatactcaactcagcgaactgtgattggtggg	709
QY	684	TTCATTGAGGGCCCCAGTGTACGCTTGTGATTCAGTGTGAGCCCTTGGAGGCCCAACCTG	743
Db	710	tactatggcccccaatgctcagcttctgtagtctgagcctcttggaggccccagaagctg	769
QY	744	GGTACCATGAGACTGTACTACACCCCTTTTGGAACTTTCACCTTCAGCTCAGCTGCTTC	803
Db	770	ggtaccacatgagactgtaccccaaccttgggaaacctcagcttcagctcagctgagtgcttc	829
QY	804	AGCTGCTCTGAAGAACAACTTAACCTGGGATTTGAGAAACCACCTGTGGACCATTTGGA	863
Db	830	agctgctctgaagaacaacttaactcagctgtgtgaagaaaccaactgtgacacattgga	889
QY	864	AACCTGGTATCTCCAGAACCAACCTGTCAAGTATTCAGTGTGAGCCTCTATCAGACCA	923
Db	890	aacttgatcatctccagaaccaactcgttcaagtgatctgtagcctctatcagcacca	949
QY	924	GATTTGGGAGATATGAACCTGTAGCCATCCCTGGCGACCTTCACGCTTAAACCTTCAGCT	983
Db	950	gatttgggagatatagaactgtcagccatccctgtgcagccttcagcttcaactctgcagctc	1009
QY	984	ACCTTCATCTGCTCGAAGAACTGATTTAATTTGGGAAGAGAAACCAATTTGTGTAATCA	1043
Db	1010	accttcacatctgctcagaagaaactgattaaatttgggaagaaabaaacatctggaatca	1069
QY	1044	TCTGGAATCTGGTCAAAATCTTAGTCCAAATATGTCAAAAATTGACAAAAGTTTCTCATG	1103
Db	1070	tcctggaatctggttcaaatctctagctcacaatgtagcaaaatctggaacaaagtcttccaa	1129
QY	1104	ATTTAAGAGAGGATTTAATTAACCCCTCTTTCATTTCCAGTGGGAGTCATGTTACTGCATTC	1163
Db	1130	atttaaggagggtgtgataataaaccctcttcatctccagtggcaggtcaatggttactgcatctc	1189
QY	1164	TCTGGGTTGGCATTTATCATTTTGGCTGCGCAAGGAGATTAAAAAAGGCAAGAAATCCAG	1223

Db 1190 tctgggttgccattatcatttgcgtgcaagagatlaaataaagcaagaatccaaag 1249  
OY 1224 AGAAGTATGAATGAGCCATATTAATGSCCTTGGTGAAGAAATTTCTTGAATACTAA 1283  
Db 1250 agaagatgaatgagccatttaacccgacctggtgaagaataattctgtgaatactaa 1309  
OY 1284 AAATCAGATGATCTTTAAATTCCTTCAGTAAAGCTTTTGTGTGGTGGACCTCTACCT 1343  
Db 1310 aatacagagatcccttaaacctccatcagaaagcttctgtgtgagaccctcctacgt 1369  
OY 1344 CAACATGAGAGTGTG-TTCCCTAGTGCATCTGGGAGAACTTTCTACCCGACCAACAGTTT 1402  
Db 1370 caaacatgaagtgcttctcctccagtcacgtggaagatcttaaccgacaaagcttc 1429  
OY 1403 CTTCAGCTTCATTTTGGCCCTCATATTTATCCCTCAACCCCGACCCACAGGTGTTATAC 1462  
Db 1430 ctccagctccatcttcgcccccatctatccctcaacccccacagcagtgcttatac 1489  
OY 1463 AGCTCAGCTTTTGTCTTCTGAGGAGAAACAAATTAAGACCAT-AAAGGAAAGATTTCA 1521  
Db 1490 agctcagcttctgtcttcttccttgagagaaacaaataagaccataaaggaaagatcca 1549  
OY 1522 TGTGAAATATTAAGATGCTGCTGCTTGTCTTGTGACTCTTGTGTTTCTGAGTTTCAATTC 1581  
Db 1550 tctggaataataaagaatgctgacttgccttcttctgacctcctgttctcagcttcaatc 1609  
OY 1582 AGTGTGCTACTGTGATGACGACACTTCTAAATGAAGTGCATTTGATACATATGTGAAT 1641  
Db 1610 agtgcgtactgtatgacagacactcccaatgaagtgcaaatctgatacataatggaat 1669  
OY 1642 ATGACATCAGCTTTTCTGTCAGATCAATTAATTCAGCTGCTTGTATACGTCGAGTAC 1701  
Db 1670 atggaactgaattctctgacagatcaaatctcagctcgtctctgatacagtcgaggtac 1729  
OY 1702 ACTCTTATAGAAGATTAATAAAGTCTACGCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCT 1761  
Db 1730 acctctatagaagaatcaaaaagctcagctcctctcttcttcttaactcagtgagtaaa 1789  
OY 1762 TGGGGCTCTCTCAAGTTGAAAGATCTATTTGACATGACCTGCGCTGTGTGAATTT 1821  
Db 1790 tgggtgtctctcgaagtgaagaagctcattgtcacgtgaagcccgctcgtctgaaatt 1849  
OY 1822 GGCACATCCATTAATTAATGCTGCTGAGGCTGCCACCTTCTTACGACCACTCTGTTTTC 1881  
Db 1850 ggcacatccatttaaacggtctca-gcctcccaactctctcagcccaactctcttcttc 1908  
OY 1882 AGTGGCTCAGTTCACACACTAGATCTCATGAGTGCACCAAGAGAGAGAGAGAGA 1941  
Db 1909 agtggctgactccacacactagcatctcagagtgccaagaagaaagagagagaga 1968  
OY 1942 AATAGCTGCGGGTCTTTTGTGGGGTCTTGTGCTGTTCTTTTATGAGACCATTC 2001  
Db 1969 aatagcctgctgtcttcttctgcttgggggttctgctgtcttcttcttcttcttcttcttct 2028  
OY 2002 CATATTTCTTAATAGTCAATGTTCTTTTATCAGATATTAATTAAGAGAAACATCACTGA 2061  
Db 2029 ctattctctatagcaaatgcttcttcttatacagatatataatlaagaaagaataacatcctga 2088  
OY 2062 AATGCTACCTCAGTGACATCTCTTTGATGTATATGGAAGATTTAAACAGAGTGGAGA 2121  
Db 2089 aatgctacgtcgaaagtgacatccctcttctgataatgaaagtgtaaaacagtgaggaga 2148  
OY 2122 AATTCCTGATTCACATGGAATGCTCTCTTCCCTTCCCTCCCGACCACTTTTATCACT 2181  
Db 2149 aatctcctgattcaaatgaatgacgtctcttctccctgcccccgagaccttcttctcact 2208  
OY 2182 TACCTAGATCTCATATCTTTTAAATTCATCTCAGGCTCCCTCAACCCGAC 2235  
Db 2209 taactagatctcaacatcttcttaaatctcactcagagctcctcctcaacccacac 2262

RESULT 6

US-60-118-318-292  
; Sequence 292, Application US/60118318  
; GENERAL INFORMATION:  
; APPLICANT: Roopa, Reddy  
; APPLICANT: Guebler, Karl, J.  
; APPLICANT: Au-Young, Janice  
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATE  
; FILE REFERENCE: PA-0013 P  
; CURRENT FILING DATE: 1999-02-01  
; NUMBER OF SEQ ID NOS: 306  
; SOFTWARE: PERL Program  
; SEQ ID NO 292  
; LENGTH: 2385  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE: -  
; OTHER INFORMATION: 1876370CB1  
US-60-118-318-292

Query Match 95.0%; Score 2146.8; DB 36; Length 2385;  
Best Local similarity 99.3%; Pred. No. 0;  
Matches 2198; Conservative 0; Mismatches 12; Indels 4; Gaps 4;  
OY 25 ACCTCGACGACACGACACCTCCCTT-GGCAAGGACCTGAGACCTTGTGCTAAGTCAAGA 83  
Db 32 acctgcagcacacacacacatccctcttggcaagagactgagacccttgcctaaagtcaga 91  
OY 84 GGCCTAATGGGCTGTCGAGGAAGACTATGAGAAGCACAAGCAAAAGCCATGATATTTCCATGG 143  
Db 92 ggtcctaatggtcgtcgacgaagaactagagaagaccaaagcaaaagcaatgatattccatg 151  
OY 144 AATATGACGACCCCAAGAGGACTTATGAAACATCTTCAAGTTGTGGGGTGGACAAATG 203  
Db 152 aaatgacagagacaccagagagactatgaaacatcttcaagtgtggtggtgagaaatg 211  
OY 204 CTCTGTGTGATTTCTTGGCAACATATGGAACCTACTGCTGAGCTTACATTAATTTGAA 263  
Db 212 cctctgtgtgattcttccttgcgacatcatagaaacgactcgtgacttcaatctctgaa 271  
OY 264 AAACCATGACATGCGCAAGGCTTAGAAGATTTGCGGAGACAATTAACACAGATTTAGTT 323  
Db 272 aaaccatgaactgcaaaaggtctagaagatcttgcgcgaacatctacaaagatttaagt 331  
OY 324 GCCATACAAAACAAGGCGAAATTTGACTATCTGAGAAAGCTGTGCCCTTCACTAGTGTCT 383  
Db 332 gccatacaaaaacaaagcggaatctgagatctctgagaaagactctgccttcagtcgtct 391  
OY 364 TACTTACTGATAGGAATCCGGAAGATAGGAGAAATATGACGCGGTGGGAACAACA 443  
Db 392 tactacttgataagaatccggaagatagagagaaatctgaaagctggtggaaacaa 451  
OY 444 TCTCTCACTGAGAGACGAGAACTGGGAGATGTGAGCCCAACACAGAGAACAAG 503  
Db 452 tctctactgaagaagaagacgtggtgagatggtgagcccaacaagaagaagaacag 511  
OY 504 GAGCATGCTGTGAGATCTATATCAAGAGAAACAAGATGACGGAATATGAAATGGAAGATGAC 563  
Db 512 gaggacgtcttgagatctcatatacagaagaaacaaagctgaaggaatggaagatgac 571  
OY 564 GCGGCGCAACAACATAAGGACACCCCTGTGTTACACAGCTTCTCCAGCCCTGGTCAATGC 623  
Db 572 ggtctgcacaacactaaagcagccctctgttacaagcttcttgcagccctggtcaatgc 631  
OY 624 AGTGGCAATGGAATGCTGTAAGAAATCATCAATTAATACACACTGTCACTGTAGTGGG 683  
Db 632 agtggcaatggaatgctgtgaataatcatcaataacacctgcaactgtgattgtggtgg 691  
OY 684 TACTATGGGCCCAATGTCACAGCTTGTGATTAAGTGTGAGGCTTTGAGGGCCGACAGCTG 743  
Db 692 tactatgggccccagtgctcagttgtgtatcagtgtagagcttcttgagggccccagagctg 751

QY 744 GGTACCATGACGTACTACCCCTTTGGAACTTCACGCTTCACAGTGTGCTTC 803  
Db 752 gttacacatgagctgtactccaccccttggaaaccttcagcttcacagtgctcttc 811  
QY 804 AGCTGCTCTGAAAGAACAACTTAACTGGGATTGAAAGAACACCTGTGGACATTTTGA 863  
Db 812 agctgctcttgaagagacaacttaacttgagatlgaaagaacacacttggacatttga 871  
QY 864 AACGCTCATGTCGACGAACAACCTGTGAGTGAATTCAGTGTGACCTGTATCAGACCA 923  
Db 872 aacgtgtacatctccagaacacacccgtcaagtgatccagtgtagccctcacagacaa 931  
QY 924 GATTGGGATCATGATGATAGCCATCCCTGGCCAGCTTCAGCTTAACTCTCATGT 983  
Db 932 gatttgggagatcatgaaactgttagccatccctggccagcttcagtttaaccttgatgt 991  
QY 984 ACCTTCATCTGCTCAGAAAGAACTGAGTTAAATGGGAAGAGAAAACCATTTGTGAATCA 1043  
Db 992 accttcatctgctcagaagagacttgatlaattgggaagaagaaaacacatttgaatca 1051  
QY 1044 TCTGGAATCTGGTCAATCTCAGTACGCAATATGTCAAAAATTTGGACAAAGTTTTCATAG 1103  
Db 1052 tctggaaactctggtcaaaacctagatccaaatcgtcaaaaaatcggacaaaagttctcaatg 1111  
QY 1104 ATTAAGAGGGTGATTAATACCCCTCTTCATTCAGTGGAGATGATGTTACTGATTC 1163  
Db 1112 attaaaggaggtgtatataaaccctcttcatccagtgtagatcgtatctgcatctc 1171  
QY 1164 TCTGGGTTGGCAATTTATCATTTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAAAG 1223  
Db 1172 tctgggttggcatctatcatcttgctcggcaaggagatlaaaaaaaggcaagaaatccaaag 1231  
QY 1224 AGAGTATGATGACCCCATTTAAATGCCCTTGGTGAAGAAATTTCTGGAATATCAAA 1283  
Db 1232 agaaagatgaatgcacacataaataacgccttggtgaagaataatctctggaaatac 1291  
QY 1284 AAATCATGAGATCTCTTAAATCTTCATGAAACGTTTGTGTGGTGACACTCTTACGT 1343  
Db 1292 aaatcatgagatctctttaaactccatccatcgaagcgttctgtgtgtgacactcttaagtc 1351  
QY 1344 CAACATGAAAGTGTG-TTCCTTTCAGTGCATCGGAGAGATTTTCAACCGACCAACAGTTTC 1402  
Db 1352 caaacatgaagtgctgtctcctcagtgatcgtggaagatcttcaaccgacaaagatctc 1411  
QY 1403 CTTCAGCTTCACATTTCCGCCCTCATTTATCCCTCAACCCCAAGGCTTTATATAC 1462  
Db 1412 cttaagcttccatctgcgccctcatctacccctcaaccccaagccacaggtgtttatcac 1471  
QY 1463 AGCTCAGCTTTTGTCTTTCTTGAGAGAAACAAATAAGACCAT-AAAGGAAGAGATTCA 1521  
Db 1472 agctcagcttctgtcttcttcgtgaggaataaataagacataaagggaagattcca 1531  
QY 1522 TGTGGAATATAAGATGGCTGACTTTGCTCTTTCTTGACGCTTGTGTTTCAATTTTC 1581  
Db 1532 tgtggaatataaagatg9ctgacttgccttcttcttgccttcttcttcaagtttcaatlc 1591  
QY 1582 AGTCTGACTTGTGATGAGACAGACATTCATAATGAAGTGAATTTGATACATATGTGAT 1641  
Db 1592 agtgcgtgaacttgatgaagacacacttcaaaatgaagtgcaaatctgtaacatacgtgac 1651  
QY 1642 ATGGAATCAGTTTCTTGACAGATCAAAATTTACGTCGCTTCTGTATACTGTGAGGATC 1701  
Db 1652 atggacatcaggttctcttcgacagatacaaatctgcgtctctctgatactctgtgaagtaac 1711  
QY 1702 ACTCTTATAGAAAGTTCAAAAAGTCTACGCTCTCTTTCTTTCTTACTCCAGTGAAGTAA 1761  
Db 1712 actcttataagaagltcaaaaaagltcacgctctcttcttcttcaactccagtgaaagtaa 1771  
QY 1762 TGGGGTCTGCTCAAGTTGGAAGAGTCTATTTTGACATGTGAGCCGCGCGCTGTGATTT 1821  
Db 1772 tggggctctgctcaagtttgaaagagtcctatcttgcacgtgagcccgcgctcgtgaaatc 1831  
QY 1822 GGACCATCTCTATTTAACTGGGCTTCAAGGCTTCCACACTTTCTTACGACCACTCTCTTTTC 1881

Db 1832 ggaaccatctatcttaacatgcttca-gccctcccaacctcttcagccacctctcttctc 1890  
QY 1882 AGTTGGCTGACTTCCACACACTGTGATCTCATATGATGCTCCAGCAAGAAAAGGAGAAAGAGA 1941  
Db 1891 agttggctgacttccacacctagcatctcaatgagtgccaaagaaagaaagaaagaa 1950  
QY 1942 AATACCTGCGGGGTTTTTAACTTTGGGGGTTTTGCTGTTTCTTTTATGACACCATTC 2001  
Db 1951 aatagccgagctgttctttagtttgggggttcttgcgttcttcttataagaaacatlc 2010  
QY 2002 CTATTTCTTATAGTCAATGTTTCTTTTATCAGATATTAATTAAGAAACATCACTGA 2061  
Db 2011 ctattcttataagtaacatgattcttcttcaacagatattatltagtaagaataacatcaga 2070  
QY 2062 AATGCTAGTCAAGTACATCTTTTGTATGTCATATGGAAGAGTTTAAAAACGCTGAGAGA 2121  
Db 2071 aatgctagctgcaagtgacatctcttcttgatgcatatlgaaagagltaaaacagtgaga 2130  
QY 2122 AATTGCTGATTCACAAATGAATGCTTCCTTCCTCCCGCCCGCCAGAACTTTATCCACT 2181  
Db 2131 aattccttgatcacaaatgaagatgctctctctcttccctcgcccgccagaaactttatcc 2190  
QY 2182 TACCTAGATTCATCATATTTCTTTAAATTTCAATCTCAGGCTTCCTCAACCCGAC 2235  
Db 2191 taccagattctcaatatcttctttaaattctcatctcagagccttccctcaacccacac 2244

RESULT 7  
US-60-172-373-15742  
; Sequence 15742, Application US/60172373  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preetl  
; APPLICANT: Diep, Dinh  
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using  
; FILE REFERENCE: GX-0006 P  
; CURRENT APPLICATION NUMBER: US/60/172.373  
; CURRENT FILING DATE: 1999-12-16  
; NUMBER OF SEQ ID NOS: 25,772  
; SOFTWARE: PERL Program  
; SEQ ID NO 15742  
; LENGTH: 2387  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 331616.2  
US-60-172-373-15742

Query Match 94.3%; Score 2129.6; DB 42; Length 2387;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 2201; Conservative 0; Mismatches 9; Indels 6; Gaps 6;  
QY 25 ACCTGCACACAA-GGACACTGCCCTTT-GGCAAGAGACCTGAGACCCCTTGTGTAAGT-CAA 81  
Db 32 accgtgcagcaaaagagacactcccttgggcaagagccctgagaccttgtctaaagttccaa 91  
QY 82 GAGGCTCAATGGGCTGCGAAGAACTAGAGAAAGCAAGCAAGCAAGCCATGATATTTCCAT 141  
Db 92 gaggtctaaatgggtctgcagaaagaaactagaagaagacaaagacatgatatctcatc 151  
QY 142 GGAATGTCAAGACACCCAGAGGACTTATGGAACATCTTCAAGTTGTGGGGTGAGCAA 201  
Db 152 ggaatgtcagaagacccagagggactatlgaaacatctcaagtgtg9gg9gvgagcaa 211  
QY 202 TGCCTCTGTGTGATTTCTGTCACATTCATGGAACCTACTGCTGACATTCATATTTCTG 261  
Db 212 tgcctctgtgtgatttctcgtcaacatcaltgaaacgagatgctgtgacttaccattatctt 271  
QY 262 AAAAACCATGAACTGCAAGAGGCTAGAGATTTCTGCGAGACAAATTAACAGATTAG 321

Db 272 aaaaaccctgaaactgcaagagctagaagattctgcgcgaagaattacacagatttag 331  
QY 322 TTGCCATMAAACAAGCGGAAATTGATCTCTGGAAGAACTCTGCCCTTTCAGTCTT 381  
Db 332 ttgccaataaacaagcggaattatctgagaaagactctgacctttagcgtt 391  
QY 382 CTCTACTGATGATGAATCCGGAAGATAGAGAGATATGAGCTGGGTGGGAACCA 441  
Db 392 cttaactgtagaagatccggaagatagaggaatatacgagctggtggaacaca 451  
QY 442 AATCTCTCAGTGAAGACGAGAACCTGGGAGATGTGACCCCAACAAGAAAGACA 501  
Db 452 aatctcactgaaagacgagaaactgggagagatggtagcccaacaagaagaaca 511  
QY 502 AGGAGACTGCGTGGAGATCTATATCAAGAAACAAGATGACGGAATATGGAACGAT 561  
Db 512 agggagagactgctgagatctatataagaagaacaagatgcaagcaatggaagat 571  
QY 562 ACGCCCTGCCAACAACATAAGGAGCCCTCTTACACAGCTTCTTGGCCAGCCGTGAT 621  
Db 572 acgcctgccaacaactaaagacagccctctgttacacagcttcttgcagccctgcat 631  
QY 622 GCAGTGCCATGAGAGATGTAGAAATCATCAATCAATCAACCTGCACTGATGTGG 681  
Db 632 gcaagtgccatgagaaatgtagaaatcatcaatcaatcaatcaatcaatcaat 691  
QY 682 GGTACTAGGCGCCAGTGAAGTCAAGCTTTCAGTCTGAGCTTTCAGGAGCCCAAG 741  
Db 692 ggtactatgagcccaagtgatctgagcttctgagcttctgagcccaagc 751  
QY 742 TGGGACCATGAGACTGTACTACCCCTTTGAAACCTTACGCTTACGCTGATGTGCT 801  
Db 752 tgggacacatgagactgtactacactcttggaaactcagctcagctcagctgagct 811  
QY 802 TCAGCTGCTGAGAGAAACAATTACGGGATTAAGAAACACACTTGGACCATTTG 861  
Db 812 tcaagctgctcgaagagacaacttaacgaggaatggaagaacacacttgagacatt 871  
QY 862 GAACTGTGATCTCCGAAACCAACTGTCAAGTATGATGATGATGATGATGATGAT 921  
Db 872 gaaactgtatctccgaagacacactgtcaagtgatgagtgagctcctacaaagac 931  
QY 922 CAGATTTGGGATCATGAATGAGCATCCCTGCCAGCTTACGCTTACCTGAT 981  
Db 932 cagatttgggatacgaactgtagcactccctggcagctcagcttcaacctgcat 991  
QY 982 GTACCTTCATGCTCAGAGAACTGAGTTAATTGGAGAAAGAAACCATTTGAT 1041  
Db 992 gtaccttcatctgcacgaagaaactgatttaattgggaagaagaacaacatctg 1051  
QY 1042 CATCTGGAATCTGTCAAATCTAGTCCAAATATGCAAAAATTGGCAAAAGTTTCT 1101  
Db 1052 catctggaatctgtaaatctctgacataatgcaaaaattggacaagaattctcaa 1111  
QY 1102 TGATTAAAGAGGGATATATTAACCCCTCTTCATTCAGTGGCAGTCAATGATAC 1161  
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Db 1172 tctctgggttggcatattatcttgcctggcgaagagatataaagaagaagaatca 1231  
QY 1222 AGAAGCATGAATGAGCCCATTAATTAATGCGCCCTTGGAAGAAATTTCTGGAAT 1281  
Db 1232 aggaagcatgaatgagcccatataatcgcccttggtaagaagaatcttggaaatct 1291  
QY 1282 AAAAATCATGAGATCTTTAAATCTTTCATGAAGAGTTTGTGGTGACCTCTCTAC 1341  
Db 1292 aaaaatcatgagatctttaaatctcttcaagaaagcttctgtgtgagacactctac 1351  
QY 1342 GTCAACATGAGATGTG-TTCTTCACTGATCTGGGAGAGATTTCTACCCGACCAAGT 1400  
Db 1400

Db 1352 gtcaaatatgaatgctgttcttccctcagtgacatctggaagaattctacatgcaacagat 1411  
QY 1401 TCTCTTACGCTTTCATTTGCGCCCTGATTTATCCCTCAACCCGACCCAGCTGTTTAT 1460  
Db 1412 tctcttccatcttccatcttgcgcctcctcattatccctcacaaccccgacccaagaggttct 1471  
QY 1461 ACAGCTCAGGTTTCTCTCTTTCTGAGAGAAACAATAATGACCAT-TAAGGAAGAGAT 1519  
Db 1472 acagctcagcttcttgccttcttctgaggaagaacaataaagacataaaggaagat 1531  
QY 1520 CATGTGGAATTAAGAGAGGCTGACTTGTCTTCTTCTTCTTCTTCTTCTTCTTCT 1579  
Db 1532 catgtggaatataaagagagctgacatcttcttcttcttcttcttcttcttcttct 1591  
QY 1580 TCAGTCTGCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1639  
Db 1592 tcaagctgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1651  
QY 1640 ATATGAGCTCAGTTTCTTCTGATGATGATGATGATGATGATGATGATGATGAT 1699  
Db 1652 atatgagctcagcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 1711  
QY 1700 ACAGCTTATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1759  
Db 1712 acagcttataagaagatcaaaaagctcagctccttcttcttcttcttcttcttct 1771  
QY 1760 AATGGGCTCTGCTCAAGTTGAAAGAGTCTTATTTTTCAGCTGAGCTTCTGATGAT 1819  
Db 1772 aatgggctctgctcagcttcaagttgaagagcttcttcttcttcttcttcttcttct 1831  
QY 1820 TTGAGCATCTTATTTTAACTGCTTCAAGGCTTCCGACCTTCTTCAAGCATCTCT 1879  
Db 1832 ttgagcatcttattttaaactgcttca-gcttcccaactcttctcagcaccctcttct 1890  
QY 1880 TCACTTGGCTGATCTCAACACTTACATCTGATGATGATGATGATGATGATGAT 1939  
Db 1891 tcacttggctgacttccacactcagcactcagcactcagcactcagcactcagcact 1950  
QY 1940 GAAATGAGCTGCGGCTTTTAACTTGGGGGCTTTCCTTCTTCTTCTTCTTCTTCT 1999  
Db 1951 gaaatgagctgctgcttcttcttcttcttcttcttcttcttcttcttcttcttct 2010  
QY 2000 TCTTATTTCTTATAGTCAATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2059  
Db 2011 tcttattcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2070  
QY 2060 GAAATGAGCTGAGTCAATCTCTTGTGATGATGATGATGATGATGATGATGAT 2119  
Db 2071 gaaatgagctgagctgagctgagctgagctgagctgagctgagctgagctgagct 2130  
QY 2120 GAAATGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2179  
Db 2131 gaaatgcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2190  
QY 2180 CTATCAGATTTCTATATTTCTTAAATTTCTATCTGAGGCTTCTTCAACCCAC 2235  
Db 2191 ctatcagatcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2246

RESULT 8  
PCT-US92-03970-1  
Sequence 1, Application PC/TUS9203970  
GENERAL INFORMATION:  
APPLICANT: Dana-Farber Cancer Institute, Inc.  
TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED CELL SURFACE  
NUMBER OF INVENTIONS: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Weingarten, Schurigin, Gagnebin & Hayes  
STREET: Ten Post Office Square  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.









FILED DATE: 15-MAY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/313,109  
FILING DATE: 21-FEB-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Heine, Holliday C.  
REGISTRATION NUMBER: 34,346  
REFERENCE/DOCKET NUMBER: DFCI-318XX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-2290  
TELEFAX: (617) 451-0313  
TELEX: 940675  
SEQUENCE FOR SEQ. ID NO. 1:  
CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: NO  
LOCATION: 53..1210  
US-08-008-459-1

Query Match 92.4%; Score 2087.6; DB 4; Length 2330;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;

QY 44 CCCTTGGCAAGGACCTAGACCCCTTGCTGCTAAGTCAAGAGGCTCAATGGCTGCAGAAAG 103  
DB 7 CCTTTGGGAGAGACCTAGACCCCTTGCTGCTAAGTCAAGAGGCTCAATGGCTGCAGAAAG 66  
QY 104 AACTAGAGAGAGACCACCAAGACCATGATATTTCCATGAAATGTCAGACACCCAGAG 163  
DB 67 AACTAGAGAGAGACCACCAAGACCATGATATTTCCATGAAATGTCAGACACCCAGAG 126  
QY 164 GCACTTATGGAACATCTTCAAGCTGTGGGGTGGACAAATGCTGTGTGTAATTTCTGTC 223  
DB 127 GCACTTATGGAACATCTTCAAGCTGTGGGGTGGACAAATGCTGTGTGTAATTTCTGTC 186  
QY 224 ACATCATGGAACCTACTGCTGACCTTACCATTTCTGGAATAAACCCTGAATGGCAAG 283  
DB 187 ACATCATGGAACCCACTGCTGACCTTACCATTTCTGGAATAAACCCTGAATGGCAAG 246  
QY 284 GGTAGAGGATTTGCCGAGACAAATTACACAGATTAGTTGCCATACAAAAACAAGGCGA 343  
DB 247 GGTAGAGGATTTGCCGAGACAAATTACACAGATTAGTTGCCATACAAAAACAAGGCGA 306  
QY 344 AATTGAGTATCTGGAAGAGACTTGCCTTCACTGCTTCTTACTACTGATAGGAATCCG 403  
DB 307 AATTGAGTATCTGGAAGAGACTTGCCTTCACTGCTTCTTACTACTGATAGGAATCCG 366  
QY 404 GAAGATAGAGGAATATGAGAGGTTGGGGGAGACCAACAATCTCTCACTAAGAGAGAGA 463  
DB 367 GAAGATAGAGGAATATGAGAGGTTGGGGGAGACCAACAATCTCTCACTAAGAGAGAGA 426  
QY 464 GAACGTGGGAGATGTTGAGCCCAACAACAAGAAAGAACAGAGGACTGCGTGGAGATCTA 523  
DB 427 GAACGTGGGAGATGTTGAGCCCAACAACAAGAAAGAACAGAGGACTGCGTGGAGATCTA 486  
QY 524 TATCAAGAGAAACAAGATATCAGAGCAAAATGGAACATGACGCTGCACAACTAAAGGC 583  
DB 487 TATCAAGAGAAACAAGATATCAGAGCAAAATGGAACATGACGCTGCACAACTAAAGGC 546  
QY 584 AGCCCTCTGTACACAGCTCTTGCCAGCCCTGTCATGAGAGGCGCATGAGAGAAATGTGT 643  
DB 547 AGCCCTCTGTGTACACAGCTCTTGCCAGCCCTGTCATGAGAGGCGCATGAGAGAAATGTGT 606  
QY 644 AGAATCATCAATTAATCAGACCTGCAACTGTGATGTGGGGTACTATAGGGGCCCAAGTGTCA 703

DB 607 AGAATCATCAATTAATCAGACCTGCAACTGTGATGTGGGGTACTATAGGGGCCCAAGTGTCA 666  
QY 704 GCTTGTGATTCAGTGTGAGCCCTTTGGAGGCCCCAGAGCTGGGTACCATGACCTACTCA 763  
DB 667 GTTGTGTGATTCAGTGTGAGCCCTTTGGAGGCCCCAGAGCTGGGTACCATGACCTACTCA 726  
QY 764 CCCCTTGGAAACCTTCACCTTACACTCAGACTCAGAGTGTGCTTACAGTGTCTGTAAGAACAA 823  
DB 727 CCCCTTGGAAACCTTCAGCTTCAACTCAGACTGTGCCCTTACAGTGTCTGTAAGAACAA 786  
QY 824 CTTAACCTGGATTTAGAGAAACCACTGTGACACTTTTGAAGTGTGATCTCCAGAAC 883  
DB 787 CTTAACCTGGATTTAGAGAAACCACTGTGACACTTTTGAAGTGTGATCTCCAGAAC 846  
QY 884 AACCTGTCAAGTATTCAGTGTGAGCCCTTATGACACCAACAGATTTGGGATCAGTAAGTGT 943  
DB 847 AACCTGTCAAGTATTCAGTGTGAGCCCTTATGACACCAAGATTTGGGATCAGTAAGTGT 906  
QY 944 TAGCCATCCCCCTGGCCAGCTTCAGCTTACCTGTGACATGTACCTTATCTGCTCAGAGAG 1003  
DB 907 TAGCCATCCCCCTGGCCAGCTTCAAGCTTACCTGTGACATGTACCTTATCTGCTCAGAGAG 966  
QY 1004 AACTGAGTTAATTTGGAGAGAGAAACCATTTGTGATCATCTGGAATCTGGTCAATCC 1063  
DB 967 AACTGAGTTAATTTGGAGAGAGAAACCATTTGTGATCATCTGGAATCTGGTCAATCC 1026  
QY 1064 TAGTCCAAATATGTCACAAAATTTGCAACAAAGTTTCTCAATGATTTAAGAGGGTATTTAA 1123  
DB 1027 TAGTCCAAATATGTCACAAAATTTGCAACAAAGTTTCTCAATGATTTAAGAGGGTATTTAA 1086  
QY 1124 CCCCTTCTATTCACAGTGTGACATGTGTACTGATCTCTGCGGTGGCTTTATATCAT 1183  
DB 1087 CCCCTTCTATTCACAGTGTGACATGTGTACTGATCTCTGCGGTGGCTTTATATCAT 1146  
QY 1184 TTGGCTGTGCAAGAGATTTAAAAAAGCAAGAAATCCAAAGAGATGATGACCCATA 1243  
DB 1147 TTGGCTGTGCAAGAGATTTAAAAAAGCAAGAAATCCAAAGAGATGATGACCCATA 1206  
QY 1244 TTAAATGCGCCCTGTGGAAGAAATTTCTGGAATTAATAATATGATGATCTTTTAA 1303  
DB 1207 TTAAATGCGCCCTGTGGAAGAAATTTCTGGAATTAATAATATGATGATCTTTTAA 1266  
QY 1304 TCCCTTCATGAAACGTTTTGTGTGTGTCACCTCTACGTCAACATGAAGTGTG-TTCC 1362  
DB 1267 TCCCTTCATGAAACGTTTTGTGTGTGTCACCTCTACGTCAACATGAAGTGTGTCC 1326  
QY 1363 TTACAGTGCATCTGTGGAGAGATTTCTACCCGACCAACAGTTCTTCAAGTTCATTCGCC 1422  
DB 1327 TTACAGTGCATCTGTGGAGAGATTTCTACCCGACCAACAGTTCTTCAAGTTCATTCACC 1386  
QY 1423 CTCATTTATCCCTCAACCCCGCCACAGGTTTATACAGCTCAGCTTTTGTCTTTT 1482  
DB 1387 CTCATTTATCCCTCAACCCCGCCACAGGTTTATACAGCTCAGCTTTTGTCTTTT 1446  
QY 1483 CTGAGAGAGAAACAATTAAGACCAT-TAAGGAAAGGATTCATGTGAATATTAAGATGGCT 1541  
DB 1447 CTGAGAGAGAAACAATTAAGACCATTAAGGAAAGGATTCATGTGAATATTAAGATGGCT 1506  
QY 1542 GACTTTGCTCTTCTTGTGACTCTTGTGTTTCACTTCAATTCAGTCTGTACTGTAGTACAG 1601  
DB 1507 GACTTTGCTCTTCTTGTGACTCTTGTGTTTCACTTCAATTCAGTCTGTACTGTAGTACAG 1566  
QY 1602 ACACCTTCAAAATGAAGTCAAAATTTGATACATATGTAATTTGACATCAGTCTTTCTTGCA 1661  
DB 1567 ACACCTTCAAAATGAAGTCAAAATTTGATACATATGTAATTTGACATCAGTCTTTCTTGCA 1626  
QY 1662 GATCAAAATTTCAAGTCTCTTCTGTATATCTGTGAGGTACACTCTTTAATAAGTTCAAA 1721  
DB 1627 GATCAAAATTTGCGCGTCTCTGTATATCTGTGAGGTACACTCTTTAATAAGTTCAAA 1680  
QY 1722 AAGTCTAGCTCTCTCTTCTTCTTCTTCACTCAGTGTGAAGTAAATGGGCTCTGCAAGTGTGA 1781  
DB 1681 AAGTCTAGCTCTCTCTTCTTCTTCTTCACTCAGTGTGAAGTAAATGGGCTCTGCAAGTGTGA 1740



QY 1782 AAGAGTCTATTTGACAGTGAAGCTCGCCGCTGTGTAATGGACCATTATTAAGTGG 1841  
1741 AAGAGTCTATTTGACAGTGAAGCTCGCCGCTGTGTAATGGACCATTATTAAGTGG 1800  
QY 1842 CTTAGAGCTCCCAACCTCTTTCAGCCACCTCTTTTTCAGTTGGCTGACTCCACAC 1901  
1801 CTTA-CGCTCCCAACCTCTTTCAGCCACCTCTTTTTCAGTTGGCTGACTCCACAC 1859  
QY 1902 TAGCATCATGAGTGAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1961  
1860 TAGCATCATGAGTGAAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1919  
QY 1962 AGTTGGGGGTTTGGCTGCTTTTTCAGTGAAGCAATCTCTATTTTTCATAGTCAATGT 2021  
1920 AGTTGGGGGTTTGGCTGCTTTTTCAGTGAAGCAATCTCTATTTTTCATAGTCAATGT 1979  
QY 2022 TTTCTTTATCAGATATTTATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2081  
1980 TTTCTTTATCAGATATTTATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2039  
QY 2082 TTTCTTTATCAGATATTTATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2141  
2040 TTTCTTTATCAGATATTTATTTAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2099  
QY 2142 AATGCT 2201  
2100 AATGCT 2159  
QY 2202 TTTAAATTTCTGAGGCTCTCTCTCAACCCAC 2235  
2160 TTTAAATTTCTGAGGCTCTCTCTCAACCCAC 2193  
Db

RESULT 11  
US-08-340-539-1  
Sequence 1, Application US/08340539  
GENERAL INFORMATION:  
APPLICANT: Tedder, Thomas F.  
APPLICANT: Kansas, Geoffrey S.  
TITLE OF INVENTION: CHIMERIC SELECTING AS SIMULTANEOUS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Weingarten, Schurigin, Gagnebin & Hayes  
STREET: Ten Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/340,539  
FILING DATE: 16-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/008,459  
FILING DATE: 25-JAN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,606  
FILING DATE: 30-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/862,483  
FILING DATE: 02-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/770,608  
FILING DATE: 03-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/737,092

FILING DATE: 29-JUL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/730,503  
FILING DATE: 08-JUL-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/700,773  
FILING DATE: 15-MAY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/313,109  
FILING DATE: 21-FEB-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Heine, Holliday C.  
REGISTRATION NUMBER: 34,346  
REFERENCE/DOCKET NUMBER: DFCI-318X  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-2290  
TELEFAX: (617) 451-0313  
TELEX: 940675  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 53..1210  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: US 07/700,773  
FILING DATE: 15-MAY-1991  
US-08-340-539-1

Query Match 92.4%; Score 2087.6; DB 7; Length 2330;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 2161; Conservative 0; Mismatches 24; Indels 9; Gaps 5;  
QY 44 CCCTTTGGCAAGACCTGAGACCTTGTGCTTAAGTCAAGAGCGCTCAATGGCTGAGAG 103  
Db 7 CCTTTGGCAAGACCTGAGACCTTGTGCTTAAGTCAAGAGCGCTCAATGGCTGAGAG 66  
QY 104 AACGAGAGAGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 163  
Db 67 AACTGAGAGAGACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 126  
QY 164 GCACTTATGGAACATCTTCAAGTTGTGGGGGTGGAATGCTGTGTGTGATTTCTGTGC 223  
Db 127 GCACCTTATGGAACATCTTCAAGTTGTGGGGGTGGAATGCTGTGTGTGATTTCTGTGC 186  
QY 224 ACATCATGCAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 283  
Db 187 ACATCATGCAACCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 246  
QY 284 GCGTAGAAGATTTGCGCGAGCAATTTACAGATTTTACTTGTGCAAAACCAAGCGCGA 343  
Db 247 GCGTAGAAGATTTGCGCGAGCAATTTACAGATTTTACTTGTGCAAAACCAAGCGCGA 306  
QY 344 AATTGAGTATGGAAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 403  
Db 307 AATTGAGTATGGAAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 366  
QY 404 GAAGATGAGAGAGATTTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 463  
Db 367 GAAGATGAGAGAGATTTGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 426  
QY 464 GAATGGGAGATGTTGAG 523  
Db 427 GAATGGGAGATGTTGAG 486  
QY 524 TATCAAGAGAGAGAGATGAG 583

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Db 487 TATCAGAGAAACAAAGATGCGAGCAATGAGCATGACCCCTGCCAACAACATAAGGC 546
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Qy 584 AGCCCTGTGTACACAGCTTCTGGCCAGCCCTGTCATGACGATGGCCATGAGAAATGTG 643
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Db 547 ACCCTGTGTACACAGCTTCTGGCCAGCCCTGTCATGACGATGGCCATGAGAAATGTG 606
    |||
Qy 644 AGAAATCATCAATTAATCAACACCTGCAACTGTGATGGGACTATGAGGCCCAAGTGTCA 703
    |||
Db 607 AGAAATCATCAATTAATTAACCTGCAACTGTGATGGGACTATGAGGCCCAAGTGTCA 666
    |||
Qy 704 GCTTGTGATGATGATGAGCCCTTGGAGGCCCAAGACCTGGTACATGATGAGTCACTCA 763
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Db 667 GTTGTGATGATGATGAGCCCTTGGAGGCCCAAGACCTGGTACATGATGAGTCACTCA 726
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Qy 764 CCCCTTGGAAATCTCAGCTCAGCTCAGCTGATGCTGATGCTGATGCTGATGCTGATG 823
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Db 727 CCCCTTGGAAATCTCAGCTCAGCTCAGCTGATGCTGATGCTGATGCTGATGCTGATG 786
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Qy 824 CTTAACTGGGATGGAAGAAACACACCTGTGACCATTTGGAACCTGTCATCTCCAGAAC 883
    |||
Db 787 CTTAACTGGGATGGAAGAAACACACCTGTGACCATTTGGAACCTGTCATCTCCAGAAC 846
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Qy 884 AACCTGTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 943
    |||
Db 847 AACCTGTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 906
    |||
Qy 944 TACCATCCCTGCGCAGCTTACGCTTACCTGCTGATGCTGATGCTGATGCTGATGCTG 1003
    |||
Db 907 TACCATCCCTGCGCAGCTTACGCTTACCTGCTGATGCTGATGCTGATGCTGATGCTG 966
    |||
Qy 1004 AACCTGATTAATTTGGGAAGAAACACATTTGTGAATCATGATGATGATGATGATGATG 1063
    |||
Db 967 AACCTGATTAATTTGGGAAGAAACACATTTGTGAATCATGATGATGATGATGATGATG 1026
    |||
Qy 1064 TACCTCAATATGCAAAATTTGGACAAAGTTTTCATATGATTAAGAGGGTGAATTA 1123
    |||
Db 1027 TACCTCAATATGCAAAATTTGGACAAAGTTTTCATATGATTAAGAGGGTGAATTA 1086
    |||
Qy 1124 CCCCTGTTCATTCAGTGGGAGTATGATGATGATGATGATGATGATGATGATGATGAT 1183
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Db 1087 CCCCTGTTCATTCAGTGGGAGTATGATGATGATGATGATGATGATGATGATGATGAT 1146
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Qy 1184 TTGGCTGGCAAGAGATTTAAAAAGGCAAGAAATCCAAAGAGATATGATGATGATGAT 1243
    |||
Db 1147 TTGGCTGGCAAGAGATTTAAAAAGGCAAGAAATCCAAAGAGATATGATGATGATGAT 1206
    |||
Qy 1244 TTTAAATGCCCTTGGTGAAGAAATTTCTTGGATTAATAAATCATGAGATCCTTTAA 1303
    |||
Db 1207 TTTAAATGCCCTTGGTGAAGAAATTTCTTGGATTAATAAATCATGAGATCCTTTAA 1266
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Qy 1304 TCTCTTCATGAAGAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1362
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Db 1267 TCTCTTCATGAAGAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1326
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Qy 1363 TTGAGTGCATCTGGGAAGATTTTACCCGACCAAGAGTTCTTCACCTTCATTTGGCC 1422
    |||
Db 1327 TTGAGTGCATCTGGGAAGATTTTACCCGACCAAGAGTTCTTCACCTTCATTTGGCC 1386
    |||
Qy 1423 CTCATTTATCCCTCAACCCCGACCCGACAGTGTATATACAGTGCAGCTTTTGTCTTT 1482
    |||
Db 1387 CTCATTTATCCCTCAACCCCGACCCGACAGTGTATATACAGTGCAGCTTTTGTCTTT 1446
    |||
Qy 1483 CTGAGGAGAAACAAATTAAGACCATTAAGGAAAGATTCATGTGAATTAAGATGGCT 1541
    |||
Db 1447 CTGAGGAGAAACAAATTAAGACCATTAAGGAAAGATTCATGTGAATTAAGATGGCT 1506
    |||
Qy 1542 GACTTTGCTCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1601
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Db 1507 GACTTTGCTCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1566
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Qy 1602 ACACCTTAAATGAAGTCAAAATTTGATACATATGATGATGATGATGATGATGATGATG 1661
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Db 1567 ACACCTTAAATGAAGTGCAAATTTGATACATATGATGATATGACATGATTTCTTCA 1626
Qy 1662 GATCAATTTACAGCTGCTCTTGTATATCTGTGAGGTACACTTATTAAGAAATTCAA 1721
Db 1627 GATCAATTTACAGCTGCTCTTGTATATCTGTGAGGTACACTTATTAAGAAATTCAA 1680
Qy 1722 AAGTCTAGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1781
Db 1681 AAGTCTAGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1740
Qy 1782 AAGTCTCTATTTGACCTGTAAGCTGCGCTGCTGTGTGAATTTGACCAATCTATTAC 1841
Db 1741 AAGTCTCTATTTGACCTGTAAGCTGCGCTGCTGTGTGAATTTGACCAATCTATTAC 1800
Qy 1842 CTTAGAGCCCTCCACCTCTTTCAGCCAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1901
Db 1801 CTTCA - GCTTCCGACCTTCTTCAAGCCAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1859
Qy 1902 TAGCATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1961
Db 1860 TAGCATCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1919
Qy 1962 AGTTGGGGGTTTGGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2021
Db 1920 AGTTGGGGGTTTGGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1979
Qy 2022 TTCTTTTATACATATTTATTTAGTAAGAAACATCACTGTAATGCTGATGATGATG 2081
Db 1980 TTCTTTTATACATATTTATTTAGTAAGAAACATCACTGTAATGCTGATGATGATG 2039
Qy 2082 TCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2141
Db 2040 TCTCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2099
Qy 2142 AATGCTCTCTTCTTCCCTGCCCCAGAACTTTATCCACTTACCTGATGATGATGATG 2201
Db 2100 AATGCTCTCTTCTTCCCTGCCCCAGAACTTTATCCACTTACCTGATGATGATGATG 2159
Qy 2202 TTTAAATTCATCTAGAGCTTCCCTCAACCCAC 2235
Db 2160 TTTAAATTCATCTAGAGCTTCCCTCAACCCAC 2193

RESULT 12
US-08-410-569-1
: Sequence 1, Application US/08410569
: GENERAL INFORMATION:
: APPLICANT: Tedder, Thomas F.
: APPLICANT: Sperlin, Olivier G.
: TITLE OF INVENTION: LEUKOCYTE ADHESION MOLECULE-1 (LAM-1)
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESS: Weingarten, Schurigin, Gagnebin & Hayes
: STREET: Ten Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/410,569
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/770,608
: FILING DATE: 03-OCT-1991
: APPLICATION NUMBER: US 07/700,773
: FILING DATE: 15-MAY-1991

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QY 2193 TACATATCTTTAAATTTTCATCTCAGGCGCTCCCTCAACCCAC 2235
Db 1620 tacatatctttaatttcattcatctcagcctccccaacccac 1662

RESULT 15
US-60-212-659-816
; Sequence 816, Application US/60212659
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000674
; CURRENT APPLICATION NUMBER: US/60/212,659
; CURRENT FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 879
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 816
; LENGTH: 3238
; TYPE: DNA
; ORGANISM: HUMAN
US-60-212-659-816

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Query Match          44.6%; Score 1006.4; DB 46; Length 3238;
Best Local Similarity 98.9%; Pred. No. 9.3e-273;
Matches 1013; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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QY 213 GATTTCTGGCACATCATGAGAACTACTGCTGACTTACATTTCTGAATAACCCATG 272
Db 1832 gatttcctggcacatcatgagaaactactgctgactttacatcttcgaaacccatg 1891
QY 273 AACTGGCAAGGGCTAGAAGATTTCGCCAGACAATTAACAGATTTAAGTCCATAGAA 332
Db 1892 aactggcaagggtagaagatttcgccagacaatttaacagatttaagtccatagaa 1951
QY 333 AACCAAGGCGGAATTGAGTATCTGGAAGAAGACTGCGCCTTCAGTCTTCTTACTACTGG 392
Db 1952 aaccaaggcggaattgagtatctggagaagactgcgcccttcagtcttactactgg 2011
QY 393 ATAGGAATCCGAGAGATGAGAGAAATATGAGCGTGGTGGAACCAACAATCTCTCACT 452
Db 2012 ataggaatccgagagatgagagaaatatgagcggtggtggaacccaacaatctctca 2071
QY 453 GAAGAAGCAGAGAACTGGGAGATGGTGAGCCCAACAAGAAGAAACAAGAGAGACTGC 512
Db 2072 gaagaagcagagaaactgggagatggtgagccccaacaagaagaaacaagagagactgc 2131
QY 513 GTGGAGATCTATATCAAGAGAAACAAAGATGACGAAATGAAACGATGACGGCTGCCAC 572
Db 2132 gtggagatctatatcaagagaaacaaagatgacgaaatgaaacgatgacggctgccac 2191
QY 573 AAATTAAGGAGCGCCTCTGTTACACAGCTTTCTTGCCAGCCCTGCTCATGCACTGGCCAT 632
Db 2192 aaattaaggagcgccctctgtttacacagctttcttggccagccctgctcatgcca 2251
QY 633 GGAGAAATGTGTAGAAATCAATTAATCAACACTGCAACTGTGATGGGGATCTAATGGG 692
Db 2252 ggagaaatgtgtagaaatcaatataatcaacactgcaactgtgattggggatcta 2311
QY 693 CCCAGTGTGAGCTGTGATTCAGTGTGAGCCTTTGGAGGCCCCAGAGCTGGGTACCATG 752
Db 2312 cccagtgtgagctgtgatttcagtgtgagcctttggagggccccaagctgggtaccatg 2371
QY 753 GACTGTACTCACCCCTTTGGAAACTTCACCTTCAGCTCAGCTCAGTGGCCCTTACGCTGCTCT 812
Db 2372 gactgtactcacccctttggaaacttcaccttcagctcagctcagctcagctcagctc 2431
QY 813 GAAGGAACAACACTTAATCTGGGATTTGAGAAACACACTGTGACCAATTTGAAACTGTGCA 872
Db 2432 gaaggaacaacacttaacttgggatttgagaaacacactgtgaccatttggaaactgtgca 2491

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QY 873 TCTCAGAACCAACCGTTCAGTATGATGAGTGTGACGCTTATAGACACAGATTGGGG 932
Db 2492 tctcagaacccaacctgtgtcaagtgatlcagtgtagcctctatcagaccagatttg999 2551
QY 933 ATTCAGAACTGTAGCCATCCCTGGCCAGCTTTCAGCTTACCTGATGATGATGATGATG 992
Db 2552 attcagaaactgtagccatccctggccagcttccagcttaccctctgcaatgaccctcatc 2611
QY 993 TGCCTAGAAGAACTGAGTTAATTTGGGAAGAAACAAATTGTGTGATCATCTGGAATC 1052
Db 2612 tgcctagaagaactgagtttaatttgggaagaaacaaattgtgtgatcatctggaatc 2671
QY 1053 TGTCTAAATCCTAGTCCAAATATGTCAAAAATGTGACAAAAGTTTCTCATGATGATTAAGCAG 1112
Db 2672 tgtctaaatcctagtcctaataatgtcaaaaatgtgacaaaagtttctcatgattaagagag 2731
QY 1113 GGTGATTTATACCCCTCTTCATTCCAGTGGCAGTGCATGTTACTGATTCATCTGCGTTG 1172
Db 2732 ggtgatttatacccctcttcttccattccagtgagtcagtcagtcttactgcatctctcggttg 2791
QY 1173 GCATTATATTTGGCTGCGCAGAGATTAAAAAGGCAAGAAATCCCAAGAAAGTATG 1232
Db 2792 gcattatatttggctgcgagagattaaaaaggcaagaaatcccaagaaagtatg 2851
QY 1233 AATG 1236
Db 2852 aatg 2855

```

Search completed: January 13, 2001, 01:14:42  
Job time: 16950 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 12, 2001, 16:03:50 ; Search time 1277.54 Seconds  
(Without alignments)  
12390.935 Million cell updates/sec

Title: US-09-119-209-1

Perfect score: 2259  
Sequence: 1 GAATTCGCACTGCTGCTGCTT.....CCGCCACGACACTGGAATTC 2259

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_est4:\*

5: gb\_est5:\*

6: gb\_est6:\*

7: gb\_est7:\*

8: gb\_est8:\*

9: gb\_est9:\*

10: gb\_est10:\*

11: gb\_est11:\*

12: gb\_est12:\*

13: gb\_est13:\*

14: gb\_est14:\*

15: gb\_est15:\*

16: gb\_est16:\*

17: gb\_est17:\*

18: gb\_est18:\*

19: gb\_est19:\*

20: gb\_est20:\*

21: gb\_est21:\*

22: gb\_est22:\*

23: gb\_est23:\*

24: gb\_est24:\*

25: gb\_est25:\*

26: gb\_est26:\*

27: gb\_est27:\*

28: gb\_est28:\*

29: gb\_est29:\*

30: gb\_est30:\*

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36: gb\_est36:\*

37: gb\_est37:\*

38: gb\_est38:\*

39: gb\_est39:\*

40: gb\_est40:\*

41: em\_estba:\*

42: em\_estfun:\*

43: em\_esthum1:\*

44: em\_esthum2:\*

45: em\_esthum3:\*

46: em\_esthum4:\*

47: em\_esthum5:\*

48: em\_esthum6:\*

49: em\_esthum7:\*

50: em\_esthum8:\*

51: em\_esthum9:\*

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53: em\_esthum11:\*

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57: em\_esthum15:\*

58: em\_esthum16:\*

59: em\_esthum17:\*

60: em\_esthum18:\*

61: em\_esthum19:\*

62: em\_esthum20:\*

63: em\_estin1:\*

64: em\_estin2:\*

65: em\_estin3:\*

66: em\_estin4:\*

67: em\_estov1:\*

68: em\_estov2:\*

69: em\_estp1:\*

70: em\_estp12:\*

71: em\_estp13:\*

72: em\_estp14:\*

73: em\_estp15:\*

74: em\_estro1:\*

75: em\_estro2:\*

76: em\_estro3:\*

77: em\_estro4:\*

78: em\_estro5:\*

79: em\_estro6:\*

80: em\_estro7:\*

81: em\_estro8:\*

82: em\_estro9:\*

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85: em\_estro12:\*

86: em\_estro13:\*

87: gb\_est41:\*

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107: gb\_est61:\*

108: gb\_est62:\*

109: gb\_est63:\*

110: gb\_est64:\*

111: em\_esthum21:\*

112: em\_esthum22:\*

113: em\_esthum23:\*

114: em\_estcom1:\*

115: em\_estcom2:\*

116: em\_estcom2:\*

117: em\_estp16:\*  
 118: em\_estp17:\*  
 119: gb\_gss26:\*  
 120: em\_estp18:\*  
 121: em\_estp19:\*  
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 123: em\_estp21:\*  
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 125: em\_estp23:\*  
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 181: gb\_est113:\*  
 182: gb\_est114:\*  
 183: gb\_est115:\*  
 184: gb\_est116:\*  
 185: gb\_est117:\*  
 186: gb\_est118:\*  
 187: gb\_est119:\*  
 188: gb\_est120:\*  
 189: gb\_est121:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

190: gb\_gss25:\*  
 191: gb\_gss26:\*  
 192: gb\_gss27:\*  
 193: gb\_gss28:\*

## SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	552.8	26.2	621	97	AM950859
2	531.4	23.5	551	90	AM408490
3	504.4	22.3	632	39	AM075834
4	426.4	18.9	575	10	AA669146
5	406.4	18.0	465	143	N72396
6	403	17.8	478	20	A1434388
7	399.8	17.7	566	23	A1694304
8	388.4	17.2	459	6	AA352567
9	377.6	16.7	416	105	BE245855
10	368.6	16.3	502	91	AM474954
11	365.6	16.2	442	146	W00575
12	361	16.0	421	105	BE246681
13	360.4	16.0	505	92	AM574886
14	352.4	15.6	479	10	AA703085
15	351.8	15.6	482	39	AM083158
16	346.2	15.3	413	142	H75293
17	318	14.1	345	18	A1274577
18	315.8	14.0	483	16	A1144344
19	309.2	13.7	346	6	AA355788
20	302.4	13.4	467	38	AM015177
21	299.6	13.3	365	105	BE241595
22	299.2	13.2	435	15	A1038133
23	295.8	13.1	342	142	H70946
24	287	12.7	390	147	W85940
25	283.6	12.6	293	6	AA355761
26	283	12.5	308	139	C01368
27	279.4	12.4	419	15	A1026163
28	278.4	12.3	453	141	H00756
29	277.4	12.3	417	15	A1040572
30	274	12.1	403	21	A1540256
31	273	12.1	350	38	AV654869
32	272.4	12.1	287	145	T28911
33	271.8	12.0	411	38	AM002179
34	271.4	12.0	274	111	BE677382
35	271.4	12.0	282	6	AA361531
36	267.4	11.8	279	6	AA355982
37	267.4	11.8	396	9	AA610748
38	266.4	11.8	394	24	A1708341
39	265	11.7	297	6	AA355250
40	252.8	11.2	382	89	AW314314
41	245.4	10.8	371	22	A1572987
42	243.4	10.8	395	143	N68943
43	222	9.8	419	141	H00662
44	216.8	9.6	351	12	AA782203
45	207	9.2	599	28	A1047443

## ALIGNMENTS

RESULT 1  
 LOCUS AM950859  
 DEFINITION EST362929 MAGE Resequences, MAGE Homo sapiens EST  
 ACCESSION AM950859  
 VERSION AM950859.1 GI:8140521  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

01-JUN-2000  
 CDNA, mRNA sequence.



REFERENCE 1 (bases 1 to 621)  
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dhanraj, S., Gaspard, R., Gay, C., Holt, I. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeatman, T. J., and

TITLE Quackenbush, J.  
JOURNAL Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray  
COMMENT Unpublished (2000)  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 3528  
Fax: 301 838 0208  
Email: johndgetlfr.org  
Plate: 20

FEATURES  
source  
1. .621  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="MAGE\_resequences\_MACA"  
/note="Vector: pBluescriptSkm"

BASE COUNT 172 a 135 c 119 g 194 t 1 others  
ORIGIN

Query Match 26.2%; Score 592.8; DB 97; Length 621;  
Best Local Similarity 99.4%; Pred. No. 4.9e-157;  
Matches 616; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1210 GCAAGAAATCCAGAGAGATGATGACCCATATTAATGCCCTGGTGAAGAAAT 1269  
DB 1 GCAAGAAATCCAGAGAGATGATGACCCATATTAATGCCCTGGTGAAGAAAT 60  
QY 1270 TCTTGGAACTAAATAATCATGAGATCCTTTAAATCCTTCATGAAGCTTTGTGTG 1329  
DB 61 TCTTGGAACTAAATAATCATGAGATCCTTTAAATCCTTCATGAAGCTTTGTGTG 120  
QY 1330 GGCACCTCTACGTCAAAACATGAAGTGTGTTCTTCAGTGCATCTGGGAATTTCTAC 1388  
DB 121 GGCACCTCTACGTCAAAACATGAAGTGTGTTCTTCAGTGCATCTGGGAATTTCTAC 180  
QY 1389 CCGACCAACAGTCTCTTCACTTCGCGCCCTCATTTATCCCTCAACCCCAAGCC 1448  
DB 181 CCGACCAACAGTCTCTTCACTTCGCGCCCTCATTTATCCCTCAACCCCAAGCC 240  
QY 1449 ACAGGTGTTATACAGCTCAGCTTTTGTCTTTCTGAGGAGAAACAATAAGACAT-A 1507  
DB 241 ACAGGTGTTATACAGCTCAGCTTTTGTCTTTCTGAGGAGAAACAATAAGACATAA 300  
QY 1508 AGGGAAGATTCATGTGGAATATAAGATGGCTGACCTTTGCTCTTTCTGACCTCTGT 1567  
DB 301 AGGGAAGATTCATGTGGAATATAAGATGGCTGACCTTTGCTCTTTCTGACCTCTGT 360  
QY 1568 TTCAGTTCAATTCAGTGTGATGATGACAGACACTTCAAAATGAAGTGAATTTG 1627  
DB 361 TTCAGTTCAATTCAGTGTGATGATGACAGACACTTCAAAATGAAGTGAATTTG 420  
QY 1628 ATACATATGTGAATGAGACTAGTTTCTTGACAGATCAAAATTCAGCTGCTCTGTA 1687  
DB 421 ATACATATGTGAATGAGACTAGTTTCTTGACAGATCAAAATTCAGCTGCTCTGTA 480  
QY 1688 TACTGTGAGAGTACACTCTTATAGAAGTCAAAAAGTCTACGCTCTCTTTCTTTCAA 1747  
DB 481 TACTGTGAGAGTACACTCTTATAGAAGTCAAAAAGTCTACGCTCTCTTTCTTTCAA 540  
QY 1748 CTCGAGTGAAGTGAAGGCTCTGCTCAAGTGAAGAGTCTATTTGACATGTAAGCTC 1807  
DB 541 CTCGAGTGAAGTGAAGGCTCTGCTCAAGTGAAGAGTCTATTTGACATGTAAGCTC 600  
QY 1808 GCCGTCTGTGAATTGACCA 1827  
||||||| |||||||

DB 601 GCCGTCTGTGAATTGACCA 620

RESULT 2  
LOCUS AW408490  
DEFINITION UI-HF-BK0-abm-g-01-UI.r1 NIH\_MGC\_36 Homo sapiens cDNA clone  
IMAGE:3056832 5', mRNA sequence.  
ACCESSION AW408490  
VERSION AW408490.1 GI:6927547  
KEYWORDS EST.  
SOURCE  
ORGANISM Homo sapiens  
human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 551)  
AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Eco RI site shown at the beginning of the sequence.  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: M.B. Soares Lab  
CDNA Library Arrayed by: M.B. Soares Lab  
DNA Sequencing by: M.B. Soares Lab  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/MLN at:  
www.bio.lnl.gov/bdbr/image/image.html  
Seq primer: M13 Forward.

FEATURES  
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1. .551  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="IMAGE:3056832"  
/clone\_lib="NIH\_MGC\_36"  
/tissue\_type="Lymph"  
/cell\_type="germinal center B cells"  
/cell\_line="MGC85"  
/lab\_host="DH10B (LTI)"  
/note="Vector: pTZ19-Pac; Site\_1: NotI; Site\_2: Eco RI;  
Constructed from size fractionated cytoplasmic mRNA  
(0.5-1.5kb). Directionally cloned. Cells provided by Louis  
M. Staudt, Ph.D. Library preparation by Maria de Fatima  
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 162 a 124 c 106 g 159 t  
ORIGIN

Query Match 23.5%; Score 531.4; DB 90; Length 551;  
Best Local Similarity 99.6%; Pred. No. 1.3e-139;  
Matches 543; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 961 GCTTACGCTTACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
DB 7 GCTTACGCTTACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 66  
QY 1021 AGAAGAAAACATTTGTGAATCATCTGAATCTGCTCAATTCCTAGTCAATATGTCAAA 1080  
DB 67 AGAAGAAAACATTTGTGAATCATCTGAATCTGCTCAATTCCTAGTCAATATGTCAAA 126  
QY 1081 AATTGACAAAAGTTTCAATGATTAAGAGAGGATTAATACCCCTCTTCAATTCAG 1140  
DB 127 AATTGACAAAAGTTTCAATGATTAAGAGAGGATTAATACCCCTCTTCAATTCAG 186  
QY 1141 TGGCAGTATGTTTCTGATCTCTGAGGTTGGATTTATCTTTGGTGGCAAGAGAT 1200  
DB 187 TGGCAGTATGTTTCTGATCTCTGAGGTTGGATTTATCTTTGGTGGCAAGAGAT 246  
QY 1201 TAAAAAAGGCAAGAAATCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1260  
DB 247 TAAAAAAGGCAAGAAATCCAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 306  
||||||| |||||||

QY 1261 AAGAAATCTTGGAAATCTAAATCATGATGATCTTTAAATCCTTCATGAACGT 1320  
 Db 307 AAGAGAAATCTTGGAAATCTAAATCATGATGATCTTTAAATCCTTCATGAACGT 366  
 QY 1321 TTGTGGGGGACCTCTAGTCAACATGATGATG- TTCTCTTCACTGATCTGGAA 1379  
 Db 367 TTGTGGGGGACCTCTAGTCAACATGATGATGATGATGATGATGATGATGATG 426  
 QY 1380 GATTTCTACCCGACCAAGTTCCTTCAGTTCATTTCCGCTTCATTTATCCTTAAC 1439  
 Db 427 GATTTCTACCCGACCAAGTTCCTTCAGTTCATTTCCGCTTCATTTATCCTTAAC 486  
 QY 1440 CCCCAGCCCAAGTGTATATACAGCTGTTTGTCTTTCTGAGAGAAACAATA 1499  
 Db 487 CCCCAGCCCAAGTGTATATACAGCTGTTTGTCTTTCTGAGAGAAACAATA 546  
 QY 1500 AGACC 1504  
 Db 547 AGACC 551  
 RESULT 3  
 AM075834/c 632 bp mRNA EST 13-OCT-1999  
 LOCUS x80c03.x1 NCI CGAP CML1 Homo sapiens cDNA clone IMAGE:2573092 3'  
 DEFINITION similar to gb:U16150\_cds1 L-SELECTIN PRECURSOR (HUMAN);, mRNA  
 accession AM075834  
 VERSION AM075834.1 GI:6030832  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 632)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert\_C.Strausberg@nih.gov  
 Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,  
 Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life  
 Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The  
 I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
 Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LINL at:  
 www-bio.ljll.gov/bdrip/image/image.html  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 147.  
 Location/Qualifiers  
 1..632  
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 /clone\_id="NCI\_CGAP\_CML1"  
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 rearrangement positive". Includes both chronic phase and  
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 /lab\_host="DH10B"  
 /note="Organ: whole blood; Vector: PCMV-SPORT6; Site: 1;  
 Salt: Site: 2; Note: Cloned unidirectionally. Primer:  
 Oligo dT. Library constructed by Life Technologies."  
 BASE COUNT 175 a 126 c 130 g 201 t  
 ORIGIN

QY 922 CAGATTGGGGATCATGACCTGATGATCCCTGGCAGCTTACTCTGCAT 981  
 Db 632 CAGATTGGGGATCATGACCTGATGATCCCTGGCAGCTTACTCTGCAT 975  
 QY 982 GTACCTTCATCTGCTCAGAGAGAGTGAATATTTGGAGAGAGAGAGAGAGAG 1041  
 Db 574 GTACCTTCATCTGCTCAGAGAGAGTGAATATTTGGAGAGAGAGAGAGAGAG 515  
 QY 1042 CATCTGGAATCTGCTCAGAGAGAGTGAATATTTGGAGAGAGAGAGAGAGAG 1101  
 Db 514 CATCTGGAATCTGCTCAGAGAGAGTGAATATTTGGAGAGAGAGAGAGAGAG 455  
 QY 1102 TGATTAGAGAGAGATTAATTAACCCCTTCATTCAGTGGAGAGAGAGAGAGAG 1161  
 Db 454 TGATTAGAGAGAGATTAATTAACCCCTTCATTCAGTGGAGAGAGAGAGAGAG 395  
 QY 1162 TCTCTGGGCTGATTTATATCTTTGCTGGCAGAGAGATTAATTAACCCCTTC 1221  
 Db 394 TCTCTGGGCTGATTTATATCTTTGCTGGCAGAGAGATTAATTAACCCCTTC 335  
 QY 1222 AGAGAGATGAGATGACCATTAATTAATCCCTGCTGGAGAGAGAGAGAGAGAG 1280  
 Db 334 AGAGAGATGAGATGACCATTAATTAATCCCTGCTGGAGAGAGAGAGAGAGAG 276  
 QY 1281 TAAATATCATGAGATCTTTAAATCCTTCATGAGAGAGAGAGAGAGAGAG 1340  
 Db 275 TAAATATCATGAGATCTTTAAATCCTTCATGAGAGAGAGAGAGAGAGAG 216  
 QY 1341 CGTCAACATGAGAGTGTG-TTCTTCAGTGCATCTGGAGAGAGAGAGAGAGAG 1399  
 Db 215 CGTCAACATGAGAGTGTG-TTCTTCAGTGCATCTGGAGAGAGAGAGAGAGAG 156  
 QY 1400 TTCTTCAGTGCATCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459  
 Db 155 TTCTTCAGTGCATCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 96  
 QY 1460 TACAGCTCAGCTTTTGTCTTTCTGGAGAGAGAGAGAGAGAGAGAGAG 1518  
 Db 95 TACAGCTCAGCTTTTGTCTTTCTGGAGAGAGAGAGAGAGAGAGAGAGAG 36  
 QY 1519 TCATGTGAGATTAAGA 1536  
 Db 35 TCATGTGAGATTAAGA 18  
 RESULT 4  
 AA669146/c 575 bp mRNA EST 20-NOV-1997  
 LOCUS ab94c05.s1 Striatogene lung (#937210) Homo sapiens cDNA clone  
 DEFINITION IMAGE:854600 3', mRNA sequence.  
 accession AA669146  
 VERSION AA669146.1 GI:2630645  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 575)  
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gelsel, G., Jost, S.,  
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin  
 White, Y., Wyllie, T., Waterston, R., Tan, F., Theisling, B.,  
 Washington University School of Medicine  
 Contact: Wilson RK  
 Unpublished (1997)  
 TITLE JOURNAL  
 COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available royalty-free through LINL; contact the  
 IMAGE Consortium (info@image.ljll.gov) for further information.

Query Match 22.3%; Score 504.4; DB 39; Length 632;  
 Best Local Similarity 94.8%; Pred. No. 6, 1e-132;  
 Matches 586; Conservative 0; Mismatches 26; Indels 6; Gaps 6;

Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 473.

FEATURES  
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1. 575  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:854600"  
/clone\_lib="Stratagene Lung (#937210)"  
/sex="male"  
/dev\_stage="72 years"  
/lab\_host="SOLR cells (kanamycin resistant)"  
/note="Organ: Lung; Vector: pBluescript SK-; Site: 1: EcoRI  
; Site: 2: XhoI; Cloned unidirectionally. Primer: Oligo  
dT, normal lung. Average insert size: 1.0 kb; Uni-ZAP XR  
Vector: -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3'  
adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3'."

BASE COUNT 197 a 90 c 146 g 142 t

ORIGIN

Query Match 18.9% Score 426.4; DB 10; Length 575;  
Best Local Similarity 98.2%; Pred. No. 8.1e-110;  
Matches 442; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

QY 1786 GTCCTATTGCACTGTAGCCCTGCCGCTGTGAATGAGACCATCTATTACATGCGCTTC 1845  
|||||  
DB 575 GTCCTATTGCACTGTAGCCCTGCCGCTGTGAATGAGACCATCTATTACATGCGCTTC 518  
QY 1846 AGGCTCTCCCACTCTTTCAGCCACCTCTCTTTTCAGTTGGCTGACTCCACACCTAGC 1905  
|||||  
DB 517 CAGCCTCCCACTCTTTCAGCCACCTCTCTTTTCAGTTGGCTGACTCCACACCTAGC 458  
QY 1906 ATCTCATGATGAGCCAGCAAAAGAGAGAGAAATGAGCCGCGCGGTTTCTTATGTT 1965  
|||||  
DB 457 ATCTCATGATGAGCCAGCAAAAGAGAGAGAAATGAGCCGCGCGTGTCTTTTATGTT 398  
QY 1966 TGGGGGTTTTGCTGCTCTTTTATGAGACCATCTCTATTCTTATATGCAATGTTCT 2025  
|||||  
DB 397 TGGGGGTTTTGCTGCTCTTTTATGAGACCATCTCTATTCTTATATGCAATGTTCT 338  
QY 2026 TTTATATCGATTTATTTAGTAAAGAAACATCATGAAATGCTAGCTGCAAGTGCATCTC 2085  
|||||  
DB 337 TTTATATCGATTTATTTAGTAAAGAAACATCATGAAATGCTAGCTGCAAGTGCATCTC 278  
QY 2086 TTTGATGTCATATGAGAGAGATTAAACAGGAGGAAATCTGATTCACAAATGAATG 2145  
|||||  
DB 277 TTTGATGTCATATGAGAGAGATTAAACAGGAGGAAATCTGATTCACAAATGAATG 218  
QY 2146 CTCTCCCTTCCCTGCCCGCAGAACTTTTATCCACTTACCTAGATTCATATTTCTTTA 2205  
|||||  
DB 217 CTCTCCCTTCCCTGCCCGCAGAACTTTTATCCACTTACCTAGATTCATATTTCTTTA 158  
QY 2206 AATTTCATCTCAGGCTCTCCTCAACCCAC 2235  
|||||  
DB 157 AATTTCATCTCAGGCTCTCCTCAACCCAC 128

RESULT 5  
N72396 465 bp mRNA EST 02-APR-1996  
LOCUS N72396  
DEFINITION yv39c11.r1 Soares fetal liver spleen INFUS Homo sapiens cDNA clone  
(HUMAN); mRNA sequence.

ACCESSION N72396  
VERSION N72396.1 GI:1229500

KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 465)  
AUTHORS Hilder, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman  
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,

Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston  
R., Williamson, A., Wohlmann, P. and Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Seq primer: reverse ET  
High quality sequence stop: 369.

FEATURES  
source

1. 465  
/organism="Homo sapiens"  
/db\_xref="GDB:3794354"  
/db\_xref="taxon:9606"  
/clone="IMAGE:245108"  
/clone\_lib="Soares fetal liver spleen INFUS"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)  
with a modified polylinker; Site: 1: Pac I; Site: 2: Eco RI;  
1st strand cDNA was primed with a Pac I - oligo(dT) primer  
[5' AACTGGAAATTTATTTAAGATCTTTTCTTTTCTTTTCTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Pac I and cloned into the Pac I  
and Eco RI sites of the modified p773 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Felicia Bonaldo."

BASE COUNT 123 a 107 c 103 g 127 t 5 others

ORIGIN

Query Match 18.0% Score 406.4; DB 143; Length 465;  
Best Local Similarity 97.6%; Pred. No. 3.6e-104;  
Matches 454; Conservative 0; Mismatches 4; Indels 7; Gaps 4;

QY 709 TGATTTCAGTGTAGACCTTTGGAGGCCCGCAGCTGGGTACCATGAGCTGATCCGCCCT 768  
|||||  
DB 4 TGATTTCAGTGTAGACCTTTGGAGG -CCAGAGCTGGGTACCATGAGCTGATCCG -CCCT 61  
QY 769 TTGGAACCTTCAGCTTACAGCTGAGCTGTGCTTACCTGCTGGAAGAACAACTTAA 828  
|||||  
DB 62 TTGGAACCTTCAGCTTCA -ATCACAGTGTGCTTACCTGCTGGAAGAACAACTTAA 120  
QY 829 CTGGATTGGAAGAACACCGCTGTGACCATTTGGAACGTGTCATTCGGAACCAACCT 888  
|||||  
DB 121 CTGGATTGGAAGAACACCGCTGTGACCATTTGGAACGTGTCATTCGGAACCAACCT 180  
QY 889 GTCAAGTGAATTCAGTGTAGACCTTATCAGCACCAGATTTGGGATCATGAATGATGAGCC 948  
|||||  
DB 181 GTCAAGTGAATTCAGTGTAGACCTTATCAGCACCAGATTTGGGATCATGAATGATGAGCC 240  
QY 949 ATCCCTGCGCAGCTTACGCTTACCTCTGCAATGTA---CTTTCATCTCTCTGAGAGA 1004  
|||||  
DB 241 ATCCCTGCGCAGCTTACGCTTACCTCTGCAATGTA---CTTTCATCTCTCTGAGAGA 300  
QY 1005 ACCTGATTAATTTGGAGAGAAACCATTTTGAATCATCTGGAATCTGTCATAAATCT 1064  
|||||  
DB 301 ACCTGATTAATTTGGAGAGAAACCATTTTGAATCATCTGGAATCTGTCATAAATCT 360  
QY 1065 AGTCCATATGTCATAAATTTGAGCAAAAGTTTCTCAATGATTTAAGAGGCTGATTATTAAC 1124  
|||||  
DB 361 AGTCCATATGTCATAAATTTGAGCAAAAGTTTCTCAATGATTTAAGAGGCTGATTATTAAC 420  
QY 1125 CCCCTCTTCATTCAGTGTGAGCATGATGTTACTGCAATCTCTGCGG 1169  
|||||  
DB 421 CCCCTCTTCATTCAGTGTGAGCATGATGTTACTGCAATCTCTGCGG 465



DB	447	ACAGAAAGAGAAATAGCCTGGCGTGTTTTGTAGTTTG6GGGTTTTGCGTTCCTTTA	388
OY	1990	TGAGACCCATTCCTATTTCTTATTAAGTCAATGTTTTCTTTTATACAGATATATTAGTAA	2049
Db	387	TGAGACCCATTCCTATTTCTTATTAAGTCAATGTTTTCTTTTATACAGATATATTAGTAA	328
OY	2050	AAACATTCATGTAATAGTGTGCTGCAAGTACATCTTTGATGTGATATGGAAGGTAA	2109
Db	327	AAACATTCATGTAATAGTGTGCTGCAAGTACATCTTTGATGTGATATGGAAGGTAA	268
OY	2110	AAACGTTGAGAGAAATTCCTTGAATTCACATGAAATGCTCTCCCTT-CCCTGCCCCAGA	2168
Db	267	AAACGTTGAGAGAAATTCCTTGAATTCACATGAAATGCTCTCCCTTCCCTGCCCCAGA	208
OY	2169	ACTTTTATTCACATTAACATGATTCATACATATATCTTTAAATTTTCAATTCAGGCTCCCTCA	2228
Db	207	CTTTTATTCACATTAACATGATTCATACATATATCTTTAAATTTTCAATTCAGGCTCCCTCA	148
OY	2229	ACCCGAC 2235	
Db	147	ACCCGAC 141	
RESULT	8		
AA352567			
LOCUS	AA352567	459 bp	mRNA
DEFINITION	EST60518	Activated T-cells XX	Homo sapiens CDNA 5' end similar to
ACCESSION	AA352567		
VERSION	AA352567.1	GI:2004887	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	1 (bases 1 to 459)		
	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fullner,R.A., Bult		
	,C., Lee,N.H., Kinkness,E.F., Weinstock,K.G., Gocayne,J.D., White		
	,O., Sutton,C., Blake,J.A., Brandon,R.C., Man-Whi,C., Clayton,R.A.,		
	Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald		
	,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodak,A.		
	Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,		
	Kelley,J.C., Liu,L.-T., Marmaros,S.M., Merrick,J.M.,		
	Moreno-Palancas,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,		
	Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,		
	Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,		
	Behararik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,		
	Dimke,D., Feng,D.-F., Fertie,A., Fischer,C., Hastings,G.A., He,M.W.		
	,Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,		
	Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L.,		
	Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Pannor		
	,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and		
	Verter,J.C.		
TITLE	Initial assessment of human gene diversity and expression patterns		
JOURNAL	based upon 83 million nucleotides of cDNA sequence		
MEDLINE	Nature 377 (6547 Suppl), 3-174 (1995)		
COMMENT	96026280		
	Other ESTs: THG172390		
	Contact: Kerlavage, AR		
	Bioinformatics		
	The Institute for Genomic Research		
	9712 Medical Center Drive, Rockville, MD 20850 USA		
	Tel: 3018699056		
	Fax: 3018699423		
	Email: arkerlav@tigr.org		
	For clone availability, additional sequence and expression		
	information related to this EST, please check the TIGR Human Gene		
	Index ( <a href="http://www.tigr.org/tdb/hgi/hgi.html">http://www.tigr.org/tdb/hgi/hgi.html</a> )		
	Seq primer: M13 Reverse.		
FEATURES	Location/Qualifiers		
SOURCE	1..459		
	"/organism="Homo sapiens"		
	"/db_xref="ATCC (Inhost):152766"		

BASE COUNT	137 a	93 c	91 g	132 t	6 others
ORIGIN					
Query Match	17.2%	Score 388.4	DB 6	Length 459	
Best Local Similarity	95.4%	Pred. No. 4.6e-99			
Matches 440	Conservative 0	Mismatches 16	Indels 5	Gaps 4	
Y	1000	AAGGAAGTGGTGAATTTGGGAAGCAAAACCATTTGTGAATCAGTCGAATCTGTCAA	1059		
Db	1	AAGGAAGTGGTGAATTTGGGAAGCAAAACCATTTGTGAATCAGTCGAATCTGTCAA	60		
Y	1060	ATTCCTAGTCCATATATGTCAAAAATTGGCAAAAAGTTTCTCAATGATTTAAGAGGGTGATT	1119		
Db	61	ATTCCTAGTCCATATATGTCAAAAATTGGCAAAAAGTTTCTCAATGATTTAAGAGGGTGATT	120		
Y	1120	ATAACCCCTCTTCATTTCCAGTGGCAGTCATGGTTTCCTGATTCCTGCGGTTGCCATTTA	1179		
Db	121	ATAACCCCTCTTCATTTCCAGTGGCAGTCATGGTTTCCTGATTCCTGCGGTTGCCATTTA	180		
Y	1180	TCATTTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAAAGACATATGATGAC	1239		
Db	181	TCATTTGGCTGGCAAGAGATTTAAAAAAGCAAGAAATCCAAAGACATATGATGAC	240		
Y	1240	CATATTTAAATGCGCCCTTGGTGAAGAAATTTCTGGAAATCTAATAATCATGATCTT	1299		
Db	241	CATATTTAAATGCGCCCTTGGTGAAGAAATTTCTGGAAATCTAATAATCATGATCTT	300		
Y	1300	TAAATTCCTTCCATGGAACGTTTTGTGTGGTGGCAGCTCCTACGTCAACATGAAGTGC	1358		
Db	301	TAAATTCCTTCCATGGAACGTTTTGTGTGGTGGCAGCTCCTACGTCAACATGAAGTGC	360		
Y	1359	TTTCCTTCAATGATGATCGGGAAGATTTCTA-CCGACCAACAG-TTCCTTCAGCTTCATT	1416		
Db	361	TTTCCTTCAATGATGATCGGGAAGATTTCTA-CCGACCAACAG-TTCCTTCAGCTTCATT	420		
Y	1417	TGCGCCCTCATTTATCCCTCAACCCCGACCGCAGAGTGT	1457		
Db	421	TTNGCCCTCATTTATCCCTCAACCCCGACCGCAGAGTGT	459		
RESULT 9					
BE245855	416 bp	mRNA	EST	13-JUL-2000	
LOCUS	TCBAP1956	pediatric pre-B cell acute lymphoblastic leukemia			
DEFINITION	Baylor-HGSC project-TCBA	Homo sapiens cDNA clone TCBAP1956, mRNA			
ACCESSION	BE245855				
VERSION	BE245855.1	GI:9097603			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 416)				
JOURNAL	Wei,Y., Tsang,Y.T.M., Mel,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D.				
COMMENT	Bouck,J., Gibbs,R.A. and Margolin,J.F.				
	Pediatric leukemia cDNA Sequencing Project				
	Unpublished (2000)				
	Contact: Dr. Judith F. Margolin				
	Human Genome Sequencing Center at Baylor College of Medicine and				
	Texas Children's Cancer Center				
	One Baylor Plaza, Houston, TX 77030, USA				
	Tel: 713 770 4536				
	Fax: 713 770 4038				
	Email: jmargin@bcm.tmc.org				
	Seq primer: M13 primer.				

FEATURES  
source

Location/Qualifiers  
1. .416  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="ncbap1956"  
/clone\_lib="Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA"  
/sex="male"  
/tissue\_type="leukopheresis"  
/cell\_type="pre-B cells"  
/dev\_stage="pediatric 2 years"  
/lab\_host="DH10B"  
/note="Vector: lambda pSB; site\_1: BamHI; site\_2: EcoRI; first strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GAGAGCTGAGCGCGCCGACGAGAG(17)VN 3'; V-A,C,G; N=A,C,G,T] and then dg tailed. Second strand was primed with a BamHI-dC primer [5'AGGAGCTCGAGCCGCGCGCCGCAATATATATAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu"

BASE COUNT 123 a 87 c 110 g 95 t 1 others  
ORIGIN

Query Match 16.7%; Score 377.6; DB 105; Length 416;  
Best Local Similarity 98.3%; Pred. No. 5.1e-96;

Matches 402; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 25 ACCTGAGACAGACACACCTCCCTT-GGCAAGACCTGAGACCTTGCTAATGCAAGA 83  
DB 9 ACCTGAGACAGACACACCTCCCTTGGCAAGACCTGAGACCTTGCTAATGCAAGA 68  
QY 84 GGCTAATGGCTGCAAGAACTAGAGAGAGCAAGCAAGCCATGATATTTTCATAG 143  
DB 69 GGCTAATGGCTGATATAAGAACTAGAGAGAGCAAGCAAGCCATGATATTTTCATAG 128  
QY 144 AATATGACAGAGACCAAGAGGACTTATGAAACATCTTCAAGTGTGGGGTGGACAATG 203  
DB 129 AATATGACAGAGACCAAGAGGACTTATGAAACATCTTCAAGTGTGGGGTGGACAATG 188  
QY 204 CTCTGTTGATTTCTTGGACATCATGACCTACTGCTGACCTTCCATATTTTCAGAA 263  
DB 189 CTCTGTTGATTTCTTGGACATCATGACCTACTGCTGACCTTCCATATTTTCAGAA 248  
QY 264 AACCCATGAACCTGGCAAGGGCTAGAAATTTGCCGAGACAAATTAACAGATTAGTT 323  
DB 249 AACCCATGAACCTGGCAAGGGCTAGAAATTTGCCGAGACAAATTAACAGATTAGTT 308  
QY 324 GCCATACAAACAGAGCGGAATAGATCTGAGAAAGACTCTGCCCTTCAGTCGTTCT 383  
DB 309 GCCATAC-AAACAGAGCGGAATAGATCTGAGAAAGACTCTGCCCTTCAGTCGTTCT 367  
QY 384 TACTACTGATAGGAATCCGAGAGATAGAGAAATATGAGCTGGGGTGG 432  
DB 368 TACTACTGATAGGAATCCGAGAGATAGAGAAATATGAGCTGGGGTGG 416

RESULT 10  
AM474954/c 502 bp mRNA EST 24-FEB-2000  
LOCUS hb01d12.x1 NCI-CGAP\_Gas4 Homo sapiens cDNA clone IMAGE:2881943 3',  
DEFINITION AM474954  
ACCESSION AM474954  
VERSION AM474954.1 GI:7045060  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 502)

AUTHORS  
TITLE  
JOURNAL  
COMMENT

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
[www.bio.linn.gov/bdrp/image/image.html](http://www.bio.linn.gov/bdrp/image/image.html)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 415.

FEATURES  
source

Location/Qualifiers  
1. .502  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2881943"  
/clone\_lib="NCI-CGAP Gas4"  
/tissue\_type="poorly differentiated adenocarcinoma with signet ring cell features"  
/lab\_host="DH10B"  
/note="Organ: stomach; Vector: pCMV-Sport6; Site\_1: SalI; site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

BASE COUNT 174 a 77 c 120 g 130 t 1 others  
ORIGIN

Query Match 16.3%; Score 368.6; DB 91; Length 502;  
Best Local Similarity 98.7%; Pred. No. 2e-93;

Matches 371; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1860 TCTTCAGCCACCTCTCTTTTTCAGTTGGCTGACTTCACACCTAGCATCATGAGTCC 1919  
DB 502 TCTTCAGCCACCTCTCTTTTTCAGTTGGCTGACTTCACACCTAGCATCATGAGTCC 443  
QY 1920 AACCAAGAGAGAGAGAGAAATAGCCTGCGGGTTTTTATGTTGGGGTTTCTG 1979  
DB 442 AACCAAGAGAGAGAGAGAAATAGCCTGCGGGTTTTTATGTTGGGGTTTCTG 383  
QY 1980 TTTCCTTTATAGACCAATTCCTATTTCTATATAGTCAATGTTCTTTATCAGATAT 2039  
DB 382 TTTCCTTTATAGACCAATTCCTATTTCTATATAGTCAATGTTCTTTATCAGATAT 323  
QY 2040 ATTAGTAAGAAACATCACTGAAATGCTAGTGAAGTGCATCTTTTATGTCATATG 2099  
DB 322 ATTAGTAAGAAACATCACTGAAATGCTAGTGAAGTGCATCTTTTATGTCATATG 263  
QY 2100 GAAGAGTTAAACAGGTGAGAAATTCCTGATTCACAAATGAATGCTCCCTTCCCT 2159  
DB 262 GAAGAGTTAAACAGGTGAGAAATTCCTGATTCACAAATGAATGCTCCCTTCCCT 203  
QY 2160 GCCCCAGACCTTTATTCACCTTACCTAGATTTCTACATTTCTTTAAATTCATCTCAG 2219  
DB 202 GCCCCAGACCTTTATTCACCTTACCTAGATTTCTACATTTCTTTAAATTCATCTCAG 143  
QY 2220 CCTCCCTCAACCCAC 2235  
DB 142 CCTCCCTCAACCCAC 127

RESULT 11  
W00575 442 bp mRNA EST 15-APR-1996  
LOCUS za70c12.r1 Soares.fetal\_lung\_NBH119W Homo sapiens cDNA clone  
DEFINITION IMAGE:297910 5' similar to PIR:S09702 S09702 leukocyte surface  
protein Leu-8 precursor, short form - human ;contains element L1

repetitive element ; mRNA sequence.

ACCESSION W00575  
VERSION W00575.1 GI:1272051  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 442)  
Hillier, L., Clark, N., Dubuque, T., Ellison, K., Hawkins, M., Holman, M., Hulman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisakis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.  
The Mashu-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
TITLE JOURNAL  
COMMENT Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: east@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
Seq primer: ETPRimer  
High quality sequence stop: 367.  
Location/Qualifiers  
1..442  
/organism="Homo sapiens"  
/db\_xref="GDB:1242832"  
/db\_xref="taxon:9606"  
/clone="IMAGE:297910"  
/clone\_lib="Soares fetal\_lung\_NbHL19W"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTACCAATCTGAGTGGAGCGCGCCCAATTTTCTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldi. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHL19W."  
BASE COUNT 121 a 94 c 81 g 143 t 3 others  
ORIGIN

Query Match 16.28; Score 365.6; DB 146; Length 442;  
Best Local Similarity 95.08; Pred. No. 1.3e-92;  
Matches 420; Conservative 0; Mismatches 16; Indels 6; Gaps 4;

QY 1282 AAAATCATGAGATCCTTTAAATCCTTCACGAACAACTTTGTGCGTGCACCTCTAC 1341  
|||||  
Db 1 AAAATCATGAGATCCTTTAAATCCTTCACGAACAACTTTGTGCGTGCACCTCTAC 60

QY 1342 GTCAACATGAGAGTGTG-TTCCTTCAAGTCAATCTGGGAAGATTTCTACCGACCAACAGT 1400  
|||||  
Db 61 GTCAACATGAGAGTGTGTTCTTCTCAGTGCATCTGGGAAGATTTCTACCTGACCAACAGT 120

QY 1401 TTCCTGAGCTTCATTTGCGCCGTCATTTATCCCTCAACCCCGACCGACAGGTTTAT 1460  
|||||  
Db 121 TTCCTGAGCTTCATTTGCGCCGTCATTTATCCCTCAACCCCGACCGACAGGTTTAT 180

QY 1461 ACACCTCAGCTTTTGTCTTTCTTGAGAGACAACAATAGACCA-TAAGGAAAGATT 1519  
|||||  
Db 181 ACACCTCAGCTTTTGTCTTTCTTGAGAGAGAAACAATAGACCAAGGAAAGATT 240

QY 1520 CATGTGAAATTAAGATGCTGACTTGTCTTCTTGAAGTCTTGTTCAGTTTCAT 1579  
|||||  
Db 241 CATGTGAAATTAAGATGCTGACTTGTCTTCTTGAAGTCTTGTTCAGTTTCAT 300

QY 1580 TCAGTGTCTACTGATGATGACAGACACTTCTAATGAGTCAAAATTTGATACATATGCA 1639  
|||||  
Db 301 TCAGTGTCTACTGATGATGACAGACACTTCTAATGAGTCAAAATTTGATACATATGCA 360

QY 1640 ATATGAGCTCACTTTTCTTTCAGATCAATCAATTCACGTCCTTCTGTACTGTGAGAGT 1699  
|||||  
Db 361 ATATGAGCTCACT-TTNTTTCAGATCAAAATTCACGTCG---TCTGTGATCTGTGAGG 416

QY 1700 ACACCTTATAGAAAGTTCAAA 1721  
|||||  
Db 417 TCACCTTATAGAAAGTNAAAA 438

RESULT 12  
BE246681  
LOCUS BE246681 421 bp mRNA EST 13-JUL-2000  
DEFINITION TCRAPIE5091 pediatric pre-B cell acute lymphoblastic leukemia  
Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBA5091, mRNA  
sequence.  
ACCESSION BE246681  
KEYWORDS BE246681.1 GI:9098430  
EST.  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 421)  
Wei, Y., Tsang, Y.T.M., Mel, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D., Bouck, J., Gibbs, R.A. and Margolin, J.F.  
Pediatric leukemia cDNA Sequencing Project  
Unpublished (2000)  
Contact: Dr. Judith F. Margolin  
Human Genome Sequencing Center at Baylor College of Medicine and  
Texas Children's Cancer Center  
One Baylor Plaza, Houston, TX 77030, USA  
Tel: 713 770 4536  
Fax: 713 770 4038  
Email: jmargin@bcmcc.org  
Seq primer: M13 primer.  
Location/Qualifiers  
1..421  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="TCBA5091"  
/clone\_lib="pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA"  
/sex="male"  
/tissue\_type="Leukopheresis"  
/cell\_type="pre-B cell"  
/dev\_stage="pediatric 2 years"  
/lab\_host="DH10B"  
/note="Vector: lambda PSB; Site\_1: BamHI; Site\_2: EcoRI;  
First strand cDNA was primed with an anchored  
XhoI-oligo(dT) primer [5'-GGAGGAGTGGAGCGCGCCGACGAGAG(T)VN  
3'-V-A-C-G; N-A-C-G-T] and then dg tailed. Second  
strand was primed with a BamHI-dc primer  
[5'-AGAGGCTCGATCCGCGCGCAATATATAT(T) 3'].  
Double-stranded cDNA was then digested with BamHI and  
XhoI and directionally cloned into the BamHI and XhoI  
sites of lambda PSB vector. Library went through one  
round of normalization. Library was constructed by Wei  
Yu"

BASE COUNT 118 a 99 c 108 g 95 t 1 others  
ORIGIN

Query Match 16.08; Score 361; DB 105; Length 421;  
Best Local Similarity 96.88; Pred. No. 2.6e-91;  
Matches 389; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

QY 25 ACCATGACAGACAGACACTCCCTTTT-GGCAAGGAGCTGAGACCCCTTGTGTAAGTCAAGA 83  
|||||

Db 10 ACCTGCACACAGCACACTCCCTTTGGGCAAGCACTAGAACCTTGTGTANCTGGTA 69  
 QY 84 GGCTCAATGGGCTGCAGAGAACTAGAGAGCAAGCAAGCCATGATATTTCCATGG 143  
 Db 70 -GCTCAATGGGCTGCAGAGAACTAGAGAGCAAGCAAGCCATGATATTTCCATGG 128  
 QY 144 AATGTAGAGACCCAGAGGAGCTTATGAGACATCTTCAAGTTGGGGTGGACAATG 203  
 Db 129 AAATGTAGAGACCCAGAGGAGCTTATGAGACATCTTCAAGTTGGGGTGGACAATG 188  
 QY 204 CTCTGTTGATTTTCCGTCAGACATCATGAACTACTGCTGGAGCTTACCATTTATTTGAA 263  
 Db 189 CTCTGTTGATTTTCCGTCAGACATCATGAACTACTGCTGGAGCTTACCATTTATTTGAA 248  
 QY 264 AAACCCATGAATCGGCAAGAGGCTAGAGATTTCTGCCGAGACATTTACACAGATTTAGTT 323  
 Db 249 AAACCCATGAATCGGCAAGAGGCTAGAGATTTCTGCCGAGACATTTACACAGATTTAGTT 308  
 QY 324 GCATACAAAACAAAGCCGGAATTTAGTATCTGGAGAGACATCTGCTTCAAGTCTTCT 383  
 Db 309 GCCATACAAAACAAAGCCGGAATTTAGTATCTGGAGAGACATCTGCTTCAAGTCTTCT 368  
 QY 384 TACTACTGATAGGAATCCGGAAGATAGAGAGATATGAGC 425  
 Db 369 TACTACTGATAGGAATCCGGAAGATAGAGAGATATGAGC 410

RESULT 13  
 AM574886 505 bp mRNA EST 15-MAR-2000  
 LOCUS AM574886/c UI-HF-BK0-abm-9-01-0-UI.s1 NIH\_MGC\_36 Homo sapiens cDNA clone  
 DEFINITION IMAGE:3056832 3', mRNA sequence.  
 ACCESSION AM574886 GI:7246425  
 VERSION AM574886.1 GI:7246425  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 505)  
 AUTHORS NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov  
 The sequence contained an oligo-dT track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: M.B. Soares Lab  
 DNA Sequencing by: M.B. Soares Lab  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/dbp/image/image.html  
 Seq primer: M13 Forward  
 POLYA=Yes.

# FEATURES

source Location/Qualifiers  
 1..505  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3056832"  
 /clone\_lib="NIH\_MGC\_36"  
 /tissue\_type="lymph"  
 /cell\_type="germinal center B cells"  
 /cell\_line="MGC85"  
 /lab\_host="DH10B (LT1)"  
 /note="Vector: p7773-PC. Site.1: NotI. Site.2: Eco RI;  
 Constructed from size fractionated cytoplasmic mRNA  
 (0.5-1.5kb). Directionally cloned. Cells provided by Louis  
 M. Staudt, Ph.D. Library preparation by Maria de Fatima  
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 170 a 77 c 113 g 145 t  
 ORIGIN  
 Query Match 16.0% Score 360.4; DB 92; Length 505;  
 Best Local Similarity 99.7% Pred. No. 4.2e-91;  
 Matches 361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1874 TCTTTTTCAGTTGGCTGCAGCTTCCACACCTAGCATCTCATGAGTCCCAAGCAAGAGAGAG 1933  
 Db 505 TCTTTTTCAGTTGGCTGCAGCTTCCACACCTAGCATCTCATGAGTCCCAAGCAAGAGAGAG 446  
 QY 1934 AAGAGAGAAATAGGCTGGCGGCTTTTATGTTGGGGGTTTCTGCTTTTATGAG 1993  
 Db 445 AAGAGAGAAATAGGCTGGCGGCTTTTATGTTGGGGGTTTCTGCTTTTATGAG 386  
 QY 1994 ACCCATTCCTATTTCTTATAGTCAATGTTTCTTTATCAGATATTTATGTAAGAAAC 2053  
 Db 385 ACCCATTCCTATTTCTTATAGTCAATGTTTCTTTATCAGATATTTATGTAAGAAAC 326  
 QY 2054 ATCACTGAATGTAGCTGCAAGTGCATCTTGTGATGCATATGAGAGATTAAACA 2113  
 Db 325 ATCACTGAATGTAGCTGCAAGTGCATCTTGTGATGCATATGAGAGATTAAACA 266  
 QY 2114 GGTGAGAAATTCCTGTGATTCACATGAATGCTTCCTTTCCCTGCCCCAGAACTTT 2173  
 Db 265 GGTGAGAAATTCCTGTGATTCACATGAATGCTTCCTTTCCCTGCCCCAGAACTTT 206  
 QY 2174 TATCCACTTACCTAGATTTCTACATATTTCAATTTCAATTCAGAGCCCTCAACCCC 2233  
 Db 205 TATCCACTTACCTAGATTTCTACATATTTCAATTTCAATTCAGAGCCCTCAACCCC 146  
 QY 2234 AC 2235  
 Db 145 AC 144

RESULT 14  
 AA703085 479 bp mRNA EST 19-DEC-1997  
 LOCUS AA703085/c 2177g04.s1 Soares\_fetal\_liver\_spleen\_1NFrs\_S1 Homo sapiens cDNA  
 DEFINITION clone IMAGE:436854 3', mRNA sequence.  
 ACCESSION AA703085  
 VERSION AA703085.1 GI:2706198  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 479)  
 AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,  
 Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Maria,M., Martin  
 J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,  
 White,Y., Wylie,T., Waterston,R. and Wilson,R.  
 WashU-NCI human EST Project  
 Unpublished (1997)  
 JOURNAL Contact: Wilson RK  
 COMMENT Washington University School of Medicine  
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: ~40m3 fwd. ET from Amersham  
 High quality sequence stop: 413.

# FEATURES

source Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="GDB:1336623"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:436854"  
 /clone\_lib="Soares\_fetal\_liver\_spleen\_1NFrs\_S1"



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/dev_string="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site.1: Pac I; Site.2: Eco RI."
This is a subtracted version of the original Soares fetal
liver spleen INETS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5'
AACCGAAGAATTAATTAAACATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

```

Query Match	15.6%	Score 352.4	DB 10	length 479
Best Local Similarity	99.7%	Pred. No. 7.7e-89		
Matches 353	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

1882 AGTTGGCTACCTCCACACCTAGCACTCTCAAGAGTGGCAACCAAAAGAGAGAGAGAGA 1941  
 479 AGTTGGCTACTCCACACCTAGCACTCTCAAGAGTGGCAACCAAAAGAGAGAGAGAGA 420

419 AATAGCCCTGCGCTGTTTTAGTTTGGGGCTTTGCTGTTTCCTTTATAGAGACCCATTTC 360

Db 359 CTAATTCCTATAGTCATGCTTTCTTTTATATCAGATATTATTAGTAAGCAAAACATCAGCTGA 300

Db 299 AATGCTAGCTGCAAGTGACATCTCTTTGATGTCATATGGAGAGTTAAACAGAGTGGAGA 240

Db 239 AATTCCCTGATTCCACATGAATGCTCTCTCTTCCCTTGCCCCCAGACCTTTATCCACT 180

Db 1.79 TACCTAGATTCTACATATTCCTTAAATTTCATCTCAGGCCCTCCCTCAACCCAC 126

AW083158/c									
LOCUS	AW083158	482 bp	mRNA	EST	14-OCT-1999				
DEFINITION	xco6ho2.xl	NCL_CGAP_Co21	Homo sapiens	cDNA clone IMAGE:2583507					

ACCESSION	AW083158	GI:6038310
VERSION	AW083158.1	
KEYWORDS	EST.	
SOURCE	human	

ORGANISM	REFERENCE
<i>Homo sapiens</i>	1 (bases 1 to 483)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	

TITLE	JOURNAL
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)	Unpublished (1997)
Tumor Gene Index	

Tel: (301) 496-1550  
Email: Robert\_Strausberg@nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Technologies, Inc. cDNA Library Arrayed by: Christa Pirange, the I.M.A.C.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center

found through the I.M.A.G.E. Consortium/LNL at:  
www.bio.llnl.gov/bdrp/image/image.html  
Seq primer: -400p from GIBCO  
High quality sequence stop: 417.  
location/Qualifiers  
1. .482

BASE COUNT	164 a	77 c	113 g	128 t
ORIGIN				

Query Match	15.6%	Score 351.8	DB 39	Length 482
Best Local Similarity	99.4%	Pred. No. 1.1e-88		
Matches 353; Conservative	0	Mismatches 2	Indels 0	Gaps 0

1881 CAGTGGCGACATTCACACCTAGCATCTCTAGAGTCCCAAGCAAAAGGAGAGAGAG 1940  
 |||||  
 482 CAGTTGGCTGACATTCACACCTAGCATCTCTAGAGTCCCAAGCAAAAGGAGAGAGAG 423

422 AATAGCCTGCGTGTATTAGTTGGGGTTTCTGTCTTATGACCCATT 363

Db 362 CCTATTTCCTATAGTCAAATGTTCTTTATTCACGATATTATTAGTAGAGAAACATCACTG 303

302 A A A T G C T A G C T G C A A G T G A C A T C T T T G A U G T C A T A T G G A A G A C T T T A A A A C A G G T G C A G 243

Dv 2181 TTTACCTAGATTTCACATATACTCTTAAATTTTCATCTCCAGGCGGCCCTCACAACCCCAC 2335

Db 242 AATTTCCTTGATTCAACAATGACTCTCTTTCCTCCCTGGCCCCGACACTTTATTCAC 183

Db 182 TTACCGATTCACATATTCTTAATTTCATCTCAGGCCCTCCCAACCCAC 128

Search completed: January 12, 2001, 20:53:46  
Job time: 17396 sec

Sat Jan 13 11:27:50 2001

us-09-119-209-1.rst

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2001, 21:39:03 ; Search time 82.3 Seconds  
(without alignments)  
154.558 Million cell updates/sec

Title: US-09-119-209-2  
Perfect score: 2116  
Sequence: 1 MIFPMKQSTQTDLMNIFKL.....WLARRLKGGKKSRSMNDPY 372

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_36:\*

1: /cgn2\_2/gcgdata/geneseq/geneseq/AA1980.DAT:\*

2: /cgn2\_2/gcgdata/geneseq/geneseq/AA1981.DAT:\*

3: /cgn2\_2/gcgdata/geneseq/geneseq/AA1982.DAT:\*

4: /cgn2\_2/gcgdata/geneseq/geneseq/AA1983.DAT:\*

5: /cgn2\_2/gcgdata/geneseq/geneseq/AA1984.DAT:\*

6: /cgn2\_2/gcgdata/geneseq/geneseq/AA1985.DAT:\*

7: /cgn2\_2/gcgdata/geneseq/geneseq/AA1986.DAT:\*

8: /cgn2\_2/gcgdata/geneseq/geneseq/AA1987.DAT:\*

9: /cgn2\_2/gcgdata/geneseq/geneseq/AA1988.DAT:\*

10: /cgn2\_2/gcgdata/geneseq/geneseq/AA1989.DAT:\*

11: /cgn2\_2/gcgdata/geneseq/geneseq/AA1990.DAT:\*

12: /cgn2\_2/gcgdata/geneseq/geneseq/AA1991.DAT:\*

13: /cgn2\_2/gcgdata/geneseq/geneseq/AA1992.DAT:\*

14: /cgn2\_2/gcgdata/geneseq/geneseq/AA1993.DAT:\*

15: /cgn2\_2/gcgdata/geneseq/geneseq/AA1994.DAT:\*

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17: /cgn2\_2/gcgdata/geneseq/geneseq/AA1996.DAT:\*

18: /cgn2\_2/gcgdata/geneseq/geneseq/AA1997.DAT:\*

19: /cgn2\_2/gcgdata/geneseq/geneseq/AA1998.DAT:\*

20: /cgn2\_2/gcgdata/geneseq/geneseq/AA1999.DAT:\*

21: /cgn2\_2/gcgdata/geneseq/geneseq/AA2000.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2116	100.0	372	14	R37960 Human Lymphocyte H
2	2116	100.0	372	14	R38908 HuLHR, Homo sapie
3	2116	100.0	372	16	R76506 Human LHR, Homo s
4	2116	100.0	372	16	R83050 Human LHR, Homo s
5	2116	100.0	372	16	R98106 Human Lymphocyte c
6	2116	100.0	372	19	W37781 Homo sapiens lymph
7	2116	100.0	372	20	W73264 Human Lymphocyte h
8	2110	99.7	371	17	R98122 Human Lymphocyte c
9	2109	99.7	371	17	R98115 Human Lymphocyte c
10	2109	99.7	371	17	R98124 Human Lymphocyte c
11	2109	99.7	372	13	R24026 Sequence of human
12	2108	99.6	371	17	R98110 Human Lymphocyte c

13	2108	99.6	371	17	R98113 Human Lymphocyte c
14	2108	99.6	371	17	R98119 Human Lymphocyte c
15	2108	99.6	372	13	R22802 Human Lymphocyte h
16	2107	99.6	371	17	R98111 Human Lymphocyte c
17	2107	99.6	371	17	R98112 Human Lymphocyte c
18	2107	99.6	371	17	R98117 Human Lymphocyte c
19	2107	99.6	371	17	R98121 Human Lymphocyte c
20	2106	99.5	372	12	R12469 Human Lymphocyte c
21	2105	99.5	371	17	R98116 Human Lymphocyte c
22	2105	99.5	371	17	R98118 Human Lymphocyte c
23	2105	99.5	371	17	R98120 Human Lymphocyte c
24	2105	99.5	371	17	R98123 Human Lymphocyte c
25	2104	99.4	371	17	R98109 Human Lymphocyte c
26	2103	99.4	371	17	R98114 Human Lymphocyte c
27	2100.5	99.3	372	17	R98133 Human Lymphocyte c
28	2099.5	99.2	371	17	R98129 Human Lymphocyte c
29	2099.5	99.2	374	17	R98131 Human Lymphocyte c
30	2099.5	99.2	374	17	R98132 Human Lymphocyte c
31	2099.5	99.2	374	17	R98134 Human Lymphocyte c
32	2099.5	99.2	374	17	R98135 Human Lymphocyte c
33	2096.5	99.1	370	17	R98127 Human Lymphocyte c
34	2096.5	99.1	370	17	R98130 Human Lymphocyte c
35	2094.5	99.0	370	17	R98126 Human Lymphocyte c
36	2094.5	99.0	370	17	R98128 Human Lymphocyte c
37	2090	98.8	369	17	R98125 Human Lymphocyte c
38	2082	98.4	385	13	R20815 Human Lymphocyte-spect
39	2082	98.4	385	17	R91442 Human Leu8 antigen
40	2082	98.4	385	19	W80452 Human Leu8 antigen
41	2082	98.4	385	20	W86199 Human Leu8 antigen
42	2076	98.1	385	14	R34197 Sequence encoded b
43	2076	98.1	385	18	W56653 L-selectin, Homo
44	2076	98.1	385	15	W21657 Human Lymphocyte-a
45	2070	97.8	385	14	R32707 LAM-1 from PLAM-1.

#### ALIGNMENTS

RESULT 1	
R37960	ID
R37960 standard; Protein; 372 AA.	
XX	AC
XX	R37960;
XX	08-OCT-1993 (first entry)
DT	Human Lymphocyte Homing Receptor.
XX	DE
XX	HuLHR: lymphocyte binding inhibition; lymphoma metastasis;
KW	transplant rejection; inflammation.
XX	OS
XX	Homo sapiens.
FT	Key
FT	Peptide
FT	Protein
FT	Domain
FT	Modified-site
FT	Modified-site
FT	Modified-site
FT	Domain
FT	Modified-site
FT	Modified-site
FT	Region
FT	Modified-site
FT	Modified-site
FT	Modified-site

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FT      Modified-site      /note="potential N-glycosylation site"
FT      246..248
FT      /note="potential N-glycosylation site"
FT      Region            /note="potential N-glycosylation site"
FT      259..317
FT      Modified-site      /label=Complement_Binding_Repeat_2
FT      271..273
FT      /note="potential N-glycosylation site"
FT      Modified-site      311..313
FT      /note="potential N-glycosylation site"
FT      333..355
FT      Domain            /label=Transmembrane_Domain
FT      /note="stop transfer sequence"
FT      Domain            356..372
FT      /label=Cytoplasmic_Domain
FT      US5216131-A.
FT      01-JUN-1993.
FT      23-FEB-1989;      89US-0315015.
FT      23-FEB-1989;      89US-0315015.
FT      31-OCT-1991;      91US-0786149.
FT      (GETH ) GENENTECH INC.
FT      Lasky LA, Rosen SD, Singer MS, Stachel SE, Yednock TA;
FT      WPI; 1993-188588/23.
FT      N-PSDB; Q43154.
FT      Human and murine lymphocyte homing receptors to treat graft
FT      rejection and inflammation - comprise carbohydrate binding,
FT      epidermal growth factor and complement binding domains
FT      Claim 1; Fig 1 and Fig 3; 32pp; English.
FT      A human peripheral blood lymphocyte cDNA library in lambda gt10 was
FT      screened with a 2.2kb EcoRI insert of the murine Me114 antigen clone
FT      (1.e. a murine LHR sequence). The largest EcoRI insert (2.2kb) was
FT      isolated and sequenced. The ORF codes for 372 amino acids with a mol.
FT      wt. of approximately 42,200. Comparison of the HUIHR amino acid
FT      sequence with the murine LHR sequence (R37961) showed a high degree
FT      of amino acid conservation in each of the LHR domains, e.g. 96% in
FT      the transmembrane domain and 83% in the carbohydrate binding domain.
FT      The LHRs could be used to compete with the normal binding of
FT      lymphocytes to lymphoid tissue to treat inflammation or graft
FT      rejection. They could also be used to control lymphoma metastasis
FT      and to treat conditions involving lymphocyte accumulation.
FT      Sequence      372 AA:

```

```

Query Match      100.0%; Score 2116; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 3 3e-141;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MIFPWKCOSTORDIWNIFKLMGWTMLCCDPLAHHTYCWYHYHSEKPMNORARRCCRDN 60
DB      1 mifpwkcstgrdlwnifkmgwtmccdfiahgtycwtyhsekmnqrrrrfrdn 60
QY      61 YTDLVAIONAKETLEYLTKTLPFSRSYYWIGIRKIGITWVGINKSLTTEAEKMGDEPN 120
DB      61 ytdlvalionaketylkytlfpsrsyywigirkgitwvgnksltteaeekmgdepn 120
QY      121 NKRKNEKCEVEIYIKRNKMDAGKMNDDACHLKALACTYASCQPMWSCSGHGCVEELINHHHC 180
DB      121 nkrknekceveiyikrnkmdagkmdachkkaalcylascqpmwscsgghgcveelinhhtc 180
QY      181 NCDVGYGPOCQVLVIOCEPLAEPLGTMCTHPGNGFSSQCAFSCSEGTNLGTIEETT 240
DB      181 ncdvgygpcqqlvlgceplaeplgtmcthpfgnfssqcafscsegtntlgtieett 240

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QY      241 GCPFGNWSPEPTGCVIOCEPLASAPDGIIMNCSPHASFSTSTACTFICSGTELTGKKK 300
DB      241 gcpfgnwspeptgcviocpeplaspdpdgiimncshplastsfstsactficsgetelgkkk 300
QY      301 TICSSGIGWSNPSPIQCLDKSFSMKIKEDYNPFIPIVAVVWTFPSGLAFIWLARLKK 360
DB      301 ticessgigwsnpspicqldksfsmkikedyndpfiipvavvwtfpsglafiwlarlkk 360
QY      361 GKSKRSMNNDY 372
DB      361 gksksrsmndpy 372
RESULT      2
ID      R38908 standard; Protein: 372 AA.
AC      R38908;
DT      11-JAN-1994 (first entry)
DE      HUIHR.
KW      Human; murine; lymphocyte; cell surface glycoprotein; homing receptor;
KW      LHR; endothelium; lymphoid tissue; signal; domain; complement binding;
KW      carbohydrate binding; epidermal growth factor-like; egf; intracellular;
KW      transmembrane binding; cytoplasmic; ligand binding partner protein;
KW      TMD; LBPP.
OS      Homo sapiens.
XX      XX
XX      Key      Location/Qualifiers
XX      FT      Peptide      20..32
XX      /note="Signal peptide"
XX      FT      Protein      39..372
XX      /note="Mature protein"
XX      FT      Domain      39..155
XX      /note="Lectin domain"
XX      FT      Domain      160..193
XX      /note="egf domain"
XX      FT      Domain      197..317
XX      /note="Complement factor binding domain"
XX      FT      Domain      333..355
XX      /note="Transmembrane binding domain"
XX      FT      Domain      356..372
XX      /note="Cytoplasmic domain"
XX      PN      US522538-A.
XX      PD      06-JUL-1993.
XX      PF      23-FEB-1989;      89US-0315015.
XX      PR      23-FEB-1989;      89US-0315015.
XX      PR      22-NOV-1989;      89US-0440625.
XX      PR      16-DEC-1991;      91US-0808122.
XX      PA      (GETH ) GENENTECH INC.
XX      PI      Capon DJ, Lasky LA;
XX      DR      WPI; 1993-226664/28.
XX      N-PSDB; Q44243.
XX      PT      New lymphocyte homing receptor immunoglobulin fusion
XX      PT      polypeptide(s) - used to inhibit binding of lymphocytes in
XX      PT      therapeutic and diagnostic uses
XX      PS      Disclosure; Fig 1; 44pp; English.
XX      CC      The sequences given in R38908-09 represent human and murine lymphocyte
XX      CC      cell surface glycoprotein (LHR) respectively. These proteins mediate
XX      CC      the binding of lymphocytes to the endothelium of lymphoid tissue. LHR

```





```

FH Key Location/Qualifiers
FT Region 1..38
FT /label= Signal region.
FT 39..155
FT Domain /label= Lectin domain.
FT 160..193
FT Domain /label= EGF domain.
FT 197..258
FT Binding-site /label= Complement binding repeat 1.
FT 259..317
FT Binding-site /label= Complement binding repeat 2.
FT 333..355
FT Domain /label= Transmembrane domain.
FT 356..372
FT Domain /label= Cytoplasmic domain.
XX
XX US5514582-A.
XX
XX 07-MAY-1996.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI: 1996-238773/24.
XX
XX N-PSDB: R98106.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX binding site of a receptor fused to Ig constant region - useful for
XX diagnosis and treatment e.g. of inflammation
XX
XX Example 2: Figure 1: 41pp: English.
XX
XX A hybrid immunoglobulin chain comprising the ligand binding site of
XX a single transmembrane receptor without an active transmembrane
XX region; fused at its C-terminus with the N-terminus of an
XX immunoglobulin constant region. The receptor is not a member of the
XX immunoglobulin super family, nor a multiple subunit polypeptide
XX encoded by discrete genes. The hybrid immunoglobulin chain combines
XX the adhesion/targeting of a ligand binding partner (LBP) with the
XX effector functions of immunoglobulin and can bind to and/or activate
XX more than one ligand. It can be used diagnostically for the in
XX vitro assay of LBP and their targets; or therapeutically to deliver
XX LBP such as toxins, enzymes, growth factors to particular cells.
XX Typical applications are as antiviral, neuromodulating and
XX immunomodulating agents, or as modulators of cell adhesion (e.g. in
XX treating graft rejection; inflammation; metastasis etc.)
XX The immunoglobulin component increases plasma half life and
XX facilitates purification while deletion of the transmembrane region
XX potentially improves aqueous solubility and removes
XX potentially immunogenic epitopes.
XX
XX Sequence 372 AA:

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Query Match 100.0%; Score 2116; DB 17; Length 372;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-141;  
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MIFPKCOSTORDLWNIFKMGWTLCCDFLAHGTTCWTVHYSEKPMNMOBARFCRDN 60
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Db 1 mlfpwkgstgfdlnkflkngwlmcdflahnglycwtlyhsekpmnwgtrarrfcfdn 60
   |||||||
QY 61 YTDLVAIQNKAIEYLEKTLPEFSRSYVWIGIRKIGCIWTWGTNKSLTLEAENMGDGEPN 120
   |||||||

```

```

Db 61 yrdlvaigqnkaieylektlpfsrsywiglirkiggiwltwvgnkslteeaenwgdgepn 120
QY 121 NKKNKEDCEIYIKRNKQAGKWNDDACHLKAALCYTASCPWSCSGHGECEITNNHTC 180
   |||||||
Db 121 nkknkedceylikrnkdaqwnddachlkaalcyltascpwscsgghgeceyllnnhtc 180
QY 181 NCDVGYGPOCLVLIQCEPLLEAPELGTMDCVHPFNGFSFSSQCAFSQSGCTMLTGEET 240
   |||||||
Db 181 ncdvgygpcqlvlqceplleapelgltmdctvpfnfssqcafsqsgctmltgleet 240
QY 241 CGPEGNMSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFTSACTFTICSEGTETIGKKK 300
   |||||||
Db 241 cgpfgnwspeptcqvliqceplsapdlgimncshplastsftactfticsegtetlgykkk 300
QY 301 TICESSGIMSNPSPIQKIDKFSMKIEGDVNPFLPTPAVWMTARSGLAFTIWLARLKK 360
   |||||||
Db 301 ticessglwsnpspicqkldksfsmkiegdynpflptpavwmtarsglaftilwlarlkk 360
QY 361 GKSKRSMNDPY 372
   |||||||
Db 361 gkkskrsmndpy 372

RESULT 6
W37781
ID W37781 standard; Protein: 372 AA.
XX
XX W37781;
XX
XX 17-AUG-1998 (first entry)
XX
XX Homo sapiens Lymphocyte homing receptor (LHR).
XX
XX Lymphocyte homing receptor; LHR; HuLHR; organ; graft; rejection;
XX treatment; inflammatory disorders; rheumatoid arthritis;
XX autoimmune diseases; lymphoma metastasis; control; lymphocyte;
XX accumulation.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
FH Key
FH Peptide
FT /note= "potential signal sequence"
FT 60..62
FT Region
FT /note= "potential N-linked glycosylation site"
FT 104..106
FT /note= "potential N-linked glycosylation site"
FT 177..179
FT Region
FT /note= "potential N-linked glycosylation site"
FT 216..218
FT Region
FT /note= "potential N-linked glycosylation site"
FT 232..234
FT /note= "potential N-linked glycosylation site"
FT 246..248
FT Region
FT /note= "potential N-linked glycosylation site"
FT 271..273
FT Region
FT /note= "potential N-linked glycosylation site"
FT 311..313
FT Region
FT /note= "potential N-linked glycosylation site"
FT 335..357
FT Domain
FT /note= "membrane anchoring domain/stop transfer"
XX
XX US5714147-A.
XX
XX 03-FEB-1998.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 19-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.

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Db 301 lceessgiwspncpckldksfsmkdegdyndpflipavmvtafsglaflilarrlkk 360  
Qy 361 GKSKSRSMNDPY 372  
|||||  
Db 361 gkskrsmndpy 372

RESULT 8  
R98122 ID R98122 standard: Protein: 371 AA.  
XX  
AC R98122:  
XX  
DT 01-NOV-1996 (first entry)  
XX  
DE Human lymphocyte cell surface glycoprotein (HLHR) variant.  
XX  
KW Immunoglobulin; transmembrane receptor; adhesion; targeting;  
KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;  
KW immunomodulator; cell adhesion; graft rejection; inflammation;  
KW metastasis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..37  
FT /label= Signal region.  
FT Domain 38..154  
FT /label= Lectin domain.  
FT Domain 159..192  
FT /label= EGF domain.  
FT Binding-site 196..257  
FT /label= Complement binding repeat 1.  
FT Binding-site 258..316  
FT /label= Complement binding repeat 2.  
FT Domain 332..354  
FT /label= Transmembrane domain.  
FT Domain 355..371  
FT /label= Cytoplasmic domain.  
XX  
PN US5514582-A.  
XX  
XX  
PD 07-MAY-1996.  
XX  
PF 23-FEB-1989: 89US-0315015.  
XX  
PR 22-NOV-1989: 89US-0440625.  
PR 23-FEB-1989: 89US-0315015.  
PR 16-DEC-1991: 91US-0808122.  
PR 08-DEC-1992: 92US-0986931.  
PR 21-JAN-1994: 94US-0185670.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Capon DJ, Lasky LA;  
XX  
DR WPI: 1996-238773/24.  
XX  
PT Nucleic acid encoding hybrid immunoglobulin comprising the ligand  
PT binding site of a receptor fused to Ig constant region - useful for  
PT diagnosis and treatment e.g. of inflammation  
XX  
PS Disclosure: Page 19; 41pp: English.

XX  
CC A hybrid immunoglobulin chain comprising the ligand binding site of  
CC a single transmembrane receptor without an active transmembrane  
CC region; fused at its C-terminus with the N-terminus of an  
CC immunoglobulin constant region. The receptor is not a member of the  
CC immunoglobulin super family, nor a multiple subunit polypeptide  
CC encoded by discrete genes. The hybrid immunoglobulin chain combines  
CC the adhesion/targeting of a ligand binding partner (LBP) with the  
CC effector functions of immunoglobulin and can bind to and/or activate  
CC more than one ligand. It can be used diagnostically for the in

CC vitro assay of LBP and their targets: or therapeutically to deliver  
CC LBP such as toxins, enzymes, growth factors to particular cells.  
CC Typical applications are as antiviral, neuromodulating and  
CC immunomodulating agents, or as modulators of cell adhesion (e.g. in  
CC treating graft rejection; Inflammation; metastasis of lymphoma etc.)  
CC The immunoglobulin component increases plasma half life and  
CC facilitates purification while deletion of the transmembrane region  
CC facilitates recovery, improves aqueous solubility and removes  
CC potentially immunogenic epitopes. Variants of the human lymphocyte  
CC cell surface glycoprotein described in R98106 are given in  
CC R98109-R98135. This variant contains an Ile288Val substitution.  
XX  
SQ Sequence 371 AA:  
XX  
Query Match 99.7%; Score 2110; DB 17; Length 371;  
Best Local Similarity 99.7%; Pred. No. 8.7e-141;  
Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 IFPMKCGSTORDLNNIFKMGMTMLCCDFLAHHGTYCWTYHSEKPMNMRARRRCRDNY 61  
|||||  
Db 1 ifpwkqgstqrdlwnifkmgwtmccdfiahnhytcwkyhsekpmmwqarrtrctdny 60  
Qy 62 TDLVAIQKAEIEYLEKTLPSRSYVWIGIRKIGITWGTNKSLEAEAMGCGEPNN 121  
|||||  
Db 61 tdlvaigkaeieylektpsrswywigirkigitwgtlnksleaeamwgdgepnn 120  
Qy 122 KKNKEDCEVETIKRNKADAGKNDACHKLAALCYTASQCPWSCSGHCEVEIINHTCN 181  
|||||  
Db 121 kknkedcevelyikrnkdagkndachkkaalcycasqpcwsqgncvcelinnhtcn 180  
Qy 182 CDVGYGPGCOLVIOCEPLAEPLGTMDCTHPGNFSSSCAFSCSGTGLTGLEETTC 241  
|||||  
Db 181 cdvgygpgcolviqceplaeplgtmdcthpgnfssscqafscsgtgltyleetc 240  
Qy 242 GPFGNWSPPTCOVIOCEPLAPDLGIMNCSHPLASFSTACTFICSEGTETIGKKKT 301  
|||||  
Db 241 gpfgnwspptcqvioceplapdlgimnchplafstfsectfvcsegtetlgykkkt 300  
Qy 302 ICESSGIWSNRPICOKLDKFSMIKEGDYNPRLIPAVAVMTARSGLAFTIILARRLKK 361  
|||||  
Db 301 lceessgiwspncpckldksfsmkdegdyndpflipavmvtafsglaflilarrlkk 360  
Qy 362 KSKSRSMNDPY 372  
|||||  
Db 361 ksksrsmndpy 371

RESULT 9  
R98115 ID R98115 standard: Protein: 371 AA.  
XX  
AC R98115:  
XX  
DT 01-NOV-1996 (first entry)  
XX  
DE Human lymphocyte cell surface glycoprotein (HLHR) variant.  
XX  
KW Immunoglobulin; transmembrane receptor; adhesion; targeting;  
KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;  
KW immunomodulator; cell adhesion; graft rejection; inflammation;  
KW metastasis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 1..37  
FT /label= Signal region.  
FT Domain 38..154  
FT /label= Lectin domain.  
FT Domain 159..192  
FT /label= EGF domain.  
FT Binding-site 196..257

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FT      Binding-site      /label= Complement binding repeat 1.
FT      258..316
FT      /label= Complement binding repeat 2.
FT      Domain      332..354
FT      /label= Transmembrane domain.
FT      Domain      355..371
FT      /label= Cytoplasmic domain.
XX
XX      US5514582-A.
XX
XX      07-MAY-1996.
XX
XX      23-FEB-1989;      89US-0315015.
XX
XX      22-NOV-1989;      89US-0440625.
XX      23-FEB-1989;      89US-0315015.
XX      16-DEC-1991;      91US-0808122.
XX      08-DEC-1992;      92US-0986931.
XX      21-JAN-1994;      94US-0185670.
XX
XX      (GETH ) GENENTECH INC.
XX
XX      Capon DJ, Lasky LA;
XX
XX      WPI: 1996-238773/24.
XX
XX      Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX      binding site of a receptor fused to Ig constant region - useful for
XX      diagnosis and treatment e.g. of inflammation
XX
XX      Disclosure: Page 19; 41pp; English.
XX
XX      A hybrid immunoglobulin chain comprising the ligand binding site of
XX      a single transmembrane receptor without an active transmembrane
XX      region; fused at its C-terminus with the N-terminus of an
XX      immunoglobulin constant region. The receptor is not a member of the
XX      immunoglobulin super family, nor a multiple subunit polypeptide
XX      encoded by discrete genes; the hybrid immunoglobulin chain combines
XX      the adhesion/targetting of a ligand binding partner (LBP) with the
XX      effector functions of immunoglobulin and can bind to and/or activate
XX      more than one ligand. It can be used diagnostically for the in
XX      vitro assay of LBP and their targets; or therapeutically to deliver
XX      LBP such as toxins, enzymes, growth factors to particularly to deliver
XX      typical applications are as antiviral, neuromodulating and
XX      immunomodulating agents, or as modulators of cell adhesion (e.g. in
XX      treating graft rejection; inflammation; metastasis of lymphoma etc.)
XX      The immunoglobulin component increases plasma half life and
XX      facilitates purification while deletion of the transmembrane region
XX      facilitates recovery, improves aqueous solubility and removes
XX      potentially immunogenic epitopes. Variants of the human lymphocyte
XX      cell surface glycoprotein described in R98106 are given in
XX      R98109-R98135. This variant contains an Ile174Leu substitution.
XX
XX      Sequence      371 AA;
XX
XX      Query Match      99.7%; Score 2109; DB 17; Length 371;
XX      Best Local Similarity 99.7%; Pred. No. 1e-140;
XX      Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB      |||||||
DB      181 cdvgyygpqclvlgqceplleapeligmdcthrpignfsfssgcatscsegnltglecttc 240
QY      242 GPFGNMSSPEPTCGVIOCEPLASAPDLGIMNCSHPLASPSFASACTFICSGTELIGKKT 301
DB      241 gpfgnmsspeptcqvlgqceplisapdlgimcsnpasfstsactficsgtel1qkkt 300
QY      302 ICESG1WSNPSPICQKLDKSFSMIRKGDYNPLFIPVAVWYTAFSGLAFITMLARRLKKG 361
DB      301 lcesg1wsnpssplcqkldksfsm1kegdynplfipvawmvtasglafitmlarrllkky 360
QY      362 KSKSRWMDPY 372
DB      361 ksksrwmdpy 371
XX
XX      RESULT 10
XX      R98124
XX      ID R98124 standard; Protein; 371 AA.
XX
XX      AC R98124;
XX
XX      DT 01-NOV-1996 (first entry)
XX
XX      DE Human lymphocyte cell surface glycoprotein (HULHR) variant.
XX
XX      KW Immunoglobulin; transmembrane receptor; adhesion; targetting;
XX      diagnosis; therapy; drug delivery; antiviral; neuromodulator;
XX      immunomodulator; cell adhesion; graft rejection; inflammation;
XX      metastasis.
XX
XX      OS Homo sapiens.
XX
XX      FH Key Location/Qualifiers
XX      FT Region 1..37
XX      FT Domain /label= Signal region.
XX      FT Domain 38..154
XX      FT Domain /label= Lectin domain.
XX      FT Domain 159..192
XX      FT Binding-site /label= EGF domain.
XX      FT 196..257
XX      FT Binding-site /label= Complement binding repeat 1.
XX      FT 258..316
XX      FT Domain /label= Complement binding repeat 2.
XX      FT Domain 332..354
XX      FT Domain /label= Transmembrane domain.
XX      FT Domain 355..371
XX      FT Domain /label= Cytoplasmic domain.
XX
XX      US5514582-A.
XX
XX      PD 07-MAY-1996.
XX
XX      PE 23-FEB-1989;      89US-0315015.
XX
XX      PR 22-NOV-1989;      89US-0440625.
XX      23-FEB-1989;      89US-0315015.
XX      16-DEC-1991;      91US-0808122.
XX      08-DEC-1992;      92US-0986931.
XX      21-JAN-1994;      94US-0185670.
XX
XX      (GETH ) GENENTECH INC.
XX
XX      PA Capon DJ, Lasky LA;
XX
XX      PI WPI: 1996-238773/24.
XX
XX      PT Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX      binding site of a receptor fused to Ig constant region - useful for
XX      diagnosis and treatment e.g. of inflammation
XX
XX      Disclosure: Page 19; 41pp; English.

```

CC A hybrid immunoglobulin chain comprising the ligand binding site of  
 CC a single transmembrane receptor without an active transmembrane  
 CC region; fused at its C-terminus with the N-terminus of an  
 CC immunoglobulin super family. The receptor is not a member of the  
 CC immunoglobulin chain constant region. The receptor is not a member of the  
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines  
 CC the adhesion/targeting of a ligand binding partner (LBP) with the  
 CC effector functions of immunoglobulin and can bind to and/or activate  
 CC more than one ligand. It can be used diagnostically for the in  
 CC vitro assay of LBP and their targets; or therapeutically for the in  
 CC LBP such as toxins, enzymes, growth factors to particular cells.  
 CC Typical applications are as antiviral, neuromodulating and  
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in  
 CC treating graft rejection; inflammation; metastasis of lymphoma etc.)  
 CC The immunoglobulin component increases plasma half life and  
 CC facilitates purification while deletion of the transmembrane region  
 CC facilitates recovery, improves aqueous solubility and removes  
 CC potentially immunogenic epitopes. Variants of the human lymphocyte  
 CC cell surface glycoprotein described in R98106 are given in  
 CC R98109-R98135. This variant contains an Ile302Leu substitution.  
 CC  
 XX  
 SO Sequence 371 AA;

Query Match 99.7%; Score 2109; DB 17; Length 371;  
 Best Local Similarity 99.7%; Pred. No. 1e-140;  
 Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFPWKCGSTQRDLMNIFKNGMTMLCCDFLAHHTGYCWTYHSKPKPMQRRRCRDNY 61  
 |||||||  
 Db 1 ifpwkcgstqrdlmnifkngmtmlccdflahhgytcwtyhsekpmwqrrarfcrdny 60  
 |||||||  
 QY 62 TDLVAIQNKAEIEYLEKTLFPRSRYWYIGIRKIGIMTWGYNKSLTEPEAVNMGDGEPNN 121  
 |||||||  
 Db 61 tdlvaionkaeieylektlfprsrywyigirkigimtwgwynkslteeeawngdgpnn 120  
 |||||||  
 QY 122 KKNKEDCEVEIYIKRNKAGKWNDDACHIKLKAALCYTASCPWSCSGHGECVEIINNHTCN 181  
 |||||||  
 Db 121 knkedcveiyikrnkagkwnddachiklkaalcyltascpwscsghgecveiinhtcn 180  
 |||||||  
 QY 182 CDVGYGGQCOLVIOGELEAPLELGTMDCTHPFGNFSSQCAFSCSGTINLTGEETTC 241  
 |||||||  
 Db 181 cdvgyggqcolviogeleaplelgtmdcthpfgnfssqcafscsgtintlgtgeettc 240  
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 QY 242 GPFGMMSPEPTCOYIOCEPTLAPDLGIMNCSHPLASFSTFACFTISEGTETLGKKKT 301  
 |||||||  
 Db 241 gpfgmmspeptcoyioceptlapdlgimnshplasfstsacftisegetelgkkt 300  
 |||||||  
 QY 302 ICESGIMSNPSPICQKLDKSFMSIKEGDYNPLETPVAVMTAFSGLAFTIWLARLKKG 361  
 :||||||  
 Db 301 icessgimsnpspicokldksfsmikegdynplepvaavmtafsglaftiwlarrlkk 360  
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 QY 362 KKSRSKNDPY 372  
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 Db 361 kkskrsmndpy 371

RESULT 11  
 R24026  
 ID R24026 standard; Protein: 372 AA.  
 XX  
 AC R24026;  
 XX  
 DT 22-NOV-1992 (first entry)  
 XX  
 DE Sequence of human lymphocyte cell surface glycoprotein  
 XX (HLHR).  
 KW Lymphocyte cell surface glycoprotein; ligand binding protein.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers

FT Peptide 1..19  
 FT Peptide 20..38  
 FT /label= signal  
 FT Modified-site 60..62  
 FT /label= potential N-linked glycosylation site  
 FT Modified-site 104..106  
 FT /label= see above  
 FT Modified-site 177..179  
 FT /label= see above  
 FT Modified-site 216..218  
 FT /label= see above  
 FT Modified-site 232..234  
 FT /label= see above  
 FT Modified-site 271..273  
 FT /label= see above  
 FT Modified-site 311..313  
 FT /label= see above  
 FT Region 333..355  
 FT /label= stop transfer sequence

PN US5116964-A.  
 XX 26-MAY-1992.  
 PD  
 XX 22-NOV-1989; 89US-0440625.  
 PF  
 XX 23-FEB-1989; 89US-0315015.  
 PR 22-NOV-1989; 89US-0440625.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Capon DJ, Lasky LA;  
 XX WPI, 1992-199589/24.  
 DR N-PSDB; Q24987.

PT Nucleic acid encoding polypeptide fusions - comprising ligand  
 PT binding partner protein and immunoglobulin chain, for use in  
 PT diagnosis and therapy  
 PS Disclosure: Fig 1-1 - 1-3; 43pp; English.

CC LHR mediates the binding of lymphocytes to the endothelium of  
 CC lymphoid tissue. Full length cDNA clones and DNA encoding the human  
 CC and the murine LHR (HLHR and MLHR, respectively) have been  
 CC identified and isolated (see Q24987 and Q24988). LHR is a  
 CC glycoprotein which contains the following protein domains: a signal  
 CC sequence, a carbohydrate binding domain, and epidermal growth  
 CC factor-like (egf) domain, at least one and preferably two complement  
 CC binding domain repeat, a transmembrane binding domain (TMD), and a  
 CC charged intracellular or cytoplasmic domain. LHR is used as the  
 CC ligand-binding partner in fusion polypeptides with an immunoglobulin,  
 CC for use in diagnosis and therapy.  
 CC  
 XX  
 SO Sequence 372 AA;

Query Match 99.7%; Score 2109; DB 13; Length 372;  
 Best Local Similarity 99.7%; Pred. No. 1e-140;  
 Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIFPWKCGSTQRDLMNIFKNGMTMLCCDFLAHHTGYCWTYHSKPKPMQRRRCRDNY 60  
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 Db 1 mifpwkcgstqrdlmnifkngmtmlccdflahhgytcwtyhsekpmwqrrarfcrdny 60  
 |||||||  
 QY 61 YTDLVAIQNKAEIEYLEKTLFPRSRYWYIGIRKIGIMTWGYNKSLTEPEAVNMGDGEPN 120  
 |||||||  
 Db 61 ytdlvaionkaeieylektlfprsrywyigirkigimtwgwynkslteeeawngdgpnn 120  
 |||||||  
 QY 121 NKNKEDCEVEIYIKRNKAGKWNDDACHIKLKAALCYTASCPWSCSGHGECVEIINNHTC 180  
 |||||||  
 Db 121 nknkedcveiyikrnkagkwnddachiklkaalcyltascpwscsghgecveiinhtc 180  
 |||||||

```

QY 181 NCDVGYGPOCQVIOCEPLAPDELGTMDCTHPFGNFSSSCAFCSCSEGNLTGIEETT 240
DB 181 ncdvgyypqcgvlvqceplaeplgtmdcthpfnfnfsfscgafscsegnltgieett 240
QY 241 GCPKRWSSPEPTQVIOCEPLAPDUGIMNCSHPLASFSTSACTFCSGTELGK 300
DB 241 gcpkgnwsspeptqvlvqceplapdugimncshplasfstsaactfcsgegtelgk 300
QY 301 TICESSGIWSNPSPICQKLDKSFMSIKRGDYNPLFIPVAVMVTAFSGLAFTIWLARRLKK 360
DB 301 ticessgiwsspicqkldksfmsikegdynplfipvavmvtafsglatfiwlarrrlkk 360
QY 361 GKSKRSNDPY 372
DB 361 gksksrsmndpy 372

RESULT 12
R98110
ID R98110 standard. Protein: 371 AA.
AC R98110;
XX
XX 01-NOV-1996 (first entry)
DE Human lymphocyte cell surface glycoprotein (HuLHR) variant.
XX
KW Immunoglobulin; transmembrane receptor; adhesion; targeting;
KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;
KW immunomodulator; cell adhesion; graft rejection; inflammation;
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..37
FT /label= Signal region.
FT Domain 38..154
FT /label= Lectin domain.
FT Domain 159..192
FT /label= EGF domain.
FT Binding-site 196..257
FT /label= Complement binding repeat 1.
FT Binding-site 258..316
FT /label= Complement binding repeat 2.
FT Domain 332..354
FT /label= Transmembrane domain.
FT Domain 355..371
FT /label= Cytoplasmic domain.
XX
XX US5514582-A.
XX
XX 07-MAY-1996.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185670.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI: 1996-238773/24.
XX
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand
XX binding site of a receptor fused to Ig constant region - useful for
XX diagnosis and treatment e.g. of inflammation
XX
XX PS Disclosure: Page 19; 41pp; English.

```

```

XX
XX A hybrid immunoglobulin chain comprising the ligand binding site of
CC a single transmembrane receptor without an active transmembrane
CC region; fused at its C-terminus with the N-terminus of an
CC immunoglobulin constant region. The receptor is not a member of the
CC immunoglobulin super family, nor a multiple subunit polypeptide
CC encoded by discrete genes. The hybrid immunoglobulin chain combines
CC the adhesion/targeting of a ligand binding partner (LBP) with the
CC effector functions of immunoglobulin and can bind to and/or activate
CC more than one ligand. It can be used diagnostically for the in
CC vitro assay of LBP and their targets; or therapeutically to deliver
CC LBP such as toxins, enzymes, growth factors to particular cells.
CC Typical applications are as antiviral, neuromodulating and
CC immunomodulating agents, or as modulators of cell adhesion (e.g. in
CC treating graft rejection; inflammation; metastasis of lymphoma etc.)
CC The immunoglobulin component increases plasma half life and
CC facilitates purification while deletion of the transmembrane region
CC potentially improves aqueous solubility and removes
CC cell surface glycoprotein epitopes. Variants of the human lymphocyte
CC R98109-R98135. This variant contains an Ala71Ser substitution.
CC
XX
SQ Sequence 371 AA:

```

```

Query Match 99.6%; Score 2108; DB 17; Length 371;
Best Local Similarity 99.7%; Pred. No. 1.2e-140;
Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 2 IFPKCOSTGQDLMNIFKLMGWTMLCCDFLAHGYCTYHSEKPMWQRRARRECRDNY 61
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DB 362 kksksrsmndpy 371

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AC R98113;
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XX 01-NOV-1996 (first entry)
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XX Human lymphocyte cell surface glycoprotein (HuLHR) variant.
XX
XX Immunoglobulin; transmembrane receptor; adhesion; targeting;
XX diagnosis; therapy; drug delivery; antiviral; neuromodulator;
XX immunomodulator; cell adhesion; graft rejection; inflammation;
XX metastasis.
XX
XX PS

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OS Homo sapiens.  
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FH Key Location/Qualifiers  
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FT /label= Signal region.  
FT Domain 38..154  
FT /label= Lectin domain.  
FT Domain 159..192  
FT /label= EGF domain.  
FT Binding-site 196..257  
FT /label= Complement binding repeat 1.  
FT Binding-site 258..316  
FT /label= Complement binding repeat 2.  
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FT Domain 355..371  
FT /label= Cytoplasmic domain.  
XX  
XX US5514582-A.  
XX  
XX 07-MAY-1996.  
XX  
XX 23-FEB-1989; 89US-0315015.  
XX  
XX 22-NOV-1989; 89US-0440625.  
XX 23-FEB-1989; 89US-0315015.  
XX 16-DEC-1991; 91US-0808122.  
XX 08-DEC-1992; 92US-0986931.  
XX 21-JAN-1994; 94US-0185670.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Capon DJ, Lasky LA;  
XX WPI: 1996-238773/24.  
XX  
XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand  
XX binding site of a receptor fused to Ig constant region - useful for  
XX diagnosis and treatment e.g. of inflammation  
XX  
XX Disclosure: Page 19; 41pp; English.  
XX  
XX A hybrid immunoglobulin chain comprising the ligand binding site of  
XX a single transmembrane receptor without an active transmembrane  
XX region: fused at its C-terminus with the N-terminus of an  
XX immunoglobulin constant region. The receptor is not a member of the  
XX immunoglobulin super family, nor a multiple subunit polypeptide  
XX encoded by discrete genes. The hybrid immunoglobulin chain combines  
XX the adhesion/targeting of a ligand binding partner (LBP) with the  
XX effector functions of immunoglobulin and can bind to and/or activate  
XX more than one ligand. It can be used diagnostically for the in  
XX vitro assay of LBP and their targets, or therapeutically to deliver  
XX LBP such as toxins, enzymes, growth factors to particular cells.  
XX Typical applications are as antiviral, neuromodulating and  
XX immunomodulating agents, or as modulators of cell adhesion (e.g. in  
XX treating graft rejection; inflammation; metastasis of lymphoma etc.)  
XX The immunoglobulin component increases plasma half life and  
XX facilitates purification while deletion of the transmembrane region  
XX facilitates recovery, improves aqueous solubility and removes  
XX potentially immunogenic epitopes. Variants of the human lymphocyte  
XX cell surface glycoprotein described in R98106 are given in  
XX R98109-R98135. This variant contains a Leu150Val substitution.  
XX  
SQ Sequence 371 AA;

Query Match 99.6%; Score 2108; DB 17; Length 371;  
Best Local Similarity 99.7%; Pred. No. 1,2e-140;  
Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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XX R98119;  
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XX 01-NOV-1996 (first entry)  
XX  
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XX  
XX Immunoglobulin: transmembrane receptor; adhesion; targeting;  
XX diagnosis; therapy; drug delivery; antiviral; neuromodulator;  
XX immunomodulator; cell adhesion; graft rejection; inflammation;  
XX metastasis.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX FH Region 1..37  
XX FT /label= Signal region.  
XX FT Domain 38..154  
XX FT /label= Lectin domain.  
XX FT Domain 159..192  
XX FT /label= EGF domain.  
XX FT Binding-site 196..257  
XX FT /label= Complement binding repeat 1.  
XX FT Binding-site 258..316  
XX FT /label= Complement binding repeat 2.  
XX FT Domain 332..354  
XX FT /label= Transmembrane domain.  
XX FT Domain 355..371  
XX FT /label= Cytoplasmic domain.  
XX  
XX US5514582-A.  
XX  
XX 07-MAY-1996.  
XX  
XX 23-FEB-1989; 89US-0315015.  
XX  
XX 22-NOV-1989; 89US-0440625.  
XX 23-FEB-1989; 89US-0315015.  
XX 16-DEC-1991; 91US-0808122.  
XX 08-DEC-1992; 92US-0986931.  
XX 21-JAN-1994; 94US-0185670.  
XX  
XX (GETH ) GENENTECH INC.  
XX

PI Capon DJ, Lasky LA;  
 XX WPI; 1996-238773/24.  
 XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand  
 PT binding site of a receptor fused to Ig constant region - useful for  
 PT diagnosis and treatment e.g. of inflammation  
 XX  
 XX  
 PS Disclosure; Page 19; 41pp; English.

CC A hybrid immunoglobulin chain comprising the ligand binding site of  
 CC a single transmembrane receptor without an active transmembrane  
 CC region; fused at its C-terminus with the N-terminus of an  
 CC immunoglobulin constant region. The receptor is not a member of the  
 CC immunoglobulin super family, nor a multiple subunit polypeptide  
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines  
 CC the adhesion/targeting of a ligand binding partner (LBP) with the  
 CC effector functions of immunoglobulin and can bind to and/or activate  
 CC more than one ligand. It can be used diagnostically for the in  
 CC vitro assay of LBP and their targets; or therapeutically to deliver  
 CC LBP such as toxins, enzymes, growth factors to particular cells.  
 CC Typical applications are as antiviral, neuromodulating and  
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in  
 CC treating graft rejection; inflammation; metastasis of lymphoma etc.)  
 CC The immunoglobulin component increases plasma half life and  
 CC facilitates purification while deletion of the transmembrane region  
 CC facilitates recovery. Improves aqueous solubility and removes  
 CC potentially immunogenic epitopes. Variants of the human lymphocyte  
 CC cell surface glycoprotein described in R98106 are given in  
 CC R98109-R98135. This variant contains a Ser226thr substitution.  
 CC  
 XX  
 SO Sequence 371 AA:

Query Match 99.6%; Score 2108; DB 17; Length 371;  
 Best Local Similarity 99.7%; Pred. No. 1.2e-140;  
 Matches 370; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IFFPKWCOSTQRJLWNIIFKMGWTMLCCPLAHGTYCWTHYSEKPMNQRARRFCRDNY 61  
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 XX AC R22802;  
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DT 01-SEP-1992 (first entry)

XX Human lymphocyte homing receptor.

XX HuLHR; LHR; binding; endothelium; immunogens; graft; organ;  
 KW rejection; inflammation; rheumatoid arthritis; lymphoma metastasis.  
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OS Homo sapiens.

XX Key Location/Qualifiers

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Query Match 99.6%; Score 2108; DB 13; Length 372;  
Best Local Similarity 99.5%; Pred. No. 1.2e-140;  
Matches 370; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MIFPKCOSTQDMLNIFKLMGWTMLCCDFLAHHGTYCTYHYSEKPMNQARRFCRDN 60  
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Db 1 mifpkcstqtdlwnlklwgtmccdfiahgtycwyhysekpmmqarrfcrdn 60  
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Search completed: January 13, 2001, 01:15:55  
Job time: 13012 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2001, 20:53:49 ; Search time 27.24 Seconds  
(without alignments)  
245.228 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	2116	100.0	372 2 US-08-513-278-2	Sequence 2, Appli
2	2116	100.0	372 5 5514582-2	Patent No. 5514582
3	2076	98.1	385 1 US-08-340-539A-2	Sequence 2, Appli
4	2076	98.1	385 2 US-08-461-592B-2	Sequence 2, Appli
5	1651	78.0	372 2 US-08-513-278-4	Sequence 4, Appli
6	1651	78.0	372 5 5514582-4	Patent No. 5514582
7	905	42.8	830 1 US-08-110-158-4	Sequence 4, Appli
8	899	42.5	830 4 PCT-US91-05059-2	Sequence 2, Appli
9	889	42.0	830 5 5378464-2	Patent No. 5378464
10	862	40.7	610 1 US-08-365-470-3	Sequence 3, Appli
11	862	40.7	610 3 US-09-209-668-19	Sequence 19, Appli
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13	814.5	38.5	484 2 US-08-252-493C-9	Sequence 9, Appli
14	814.5	38.5	484 3 US-09-276-197-9	Sequence 9, Appli
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16	587	27.0	119 1 US-08-340-539A-14	Sequence 14, Appli
17	572	27.0	119 1 US-08-340-539A-12	Sequence 12, Appli
18	569	26.9	119 1 US-08-340-539A-13	Sequence 13, Appli
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21	467	22.1	119 1 US-08-340-539A-18	Sequence 18, Appli
22	457	22.1	119 1 US-08-340-539A-17	Sequence 17, Appli
23	452	21.4	119 1 US-08-340-539A-16	Sequence 16, Appli
24	451	21.3	119 1 US-08-340-539A-19	Sequence 19, Appli
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28	427	20.2	119 1 US-08-340-539A-15	Sequence 15, Appli

29	337	15.9	574 5 5378464-3	Patent No. 5378464
30	237	11.2	67 3 US-08-840-062-8	Sequence 8, Appli
31	199	9.4	36 1 US-08-340-539A-22	Sequence 22, Appli
32	189.5	9.0	1019 1 US-08-296-014A-4	Sequence 4, Appli
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39	177	8.4	36 1 US-08-340-539A-20	Sequence 20, Appli
40	175.5	8.3	216 3 5256642-6	Patent No. 5256642
41	172	8.1	1466 5 5472939-6	Patent No. 5472939
42	172	8.1	1466 5 5472939-5	Patent No. 5472939
43	172	8.1	1537 5 5472939-5	Patent No. 5472939
44	172	8.1	1537 5 5472939-5	Patent No. 5472939
45	172	8.1	1847 5 5256642-10	Patent No. 5256642

#### ALIGNMENTS

RESULT 1  
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Sequence 2, Application US/08513278  
Patent No. 5840844  
GENERAL INFORMATION:  
APPLICANT: LASKY, LAURENCE A.  
APPLICANT: STACHELL, SCOTT E.  
APPLICANT: ROSEN, STEVEN D.  
APPLICANT: SINGER, MARK S.  
APPLICANT: YEDNOCK, TED A.  
TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 KB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,278  
FILING DATE: 10-AUG-1995  
CLASSIFICATION: 5530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/059027  
FILING DATE: 06-MAY-1993  
APPLICATION NUMBER: 07/786149  
FILING DATE: 31-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/315015  
FILING DATE: 23-FEB-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreger, Ginger R.  
REGISTRATION NUMBER: 33,055  
REFERENCE/DOCKET NUMBER: 565D1C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-3216  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 372 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-513-278-2

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Query Match          100.0%; Score 2116; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.3e-185;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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; Patent No. 5514582
; APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
; IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 43
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185, 670
; FILING DATE: 21-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 986, 931 -
; FILING DATE: 08-DEC-1992
; APPLICATION NUMBER: 808, 122
; FILING DATE: 16-DEC-1991
; APPLICATION NUMBER: 440, 625
; FILING DATE: 22-NOV-1989
; APPLICATION NUMBER: 315, 015
; FILING DATE: 23-FEB-1989
; SEQ ID NO: 2:
; LENGTH: 372
5514582-2

Query Match          100.0%; Score 2116; DB 5; Length 372;
Best Local Similarity 100.0%; Pred. No. 2.3e-185;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 NCDVGYGPQCQLVIOCEPLAEPLGTMDCTHPFGNFSFSSQCAFSCSEGTNLGTIEETT 240
Db 181 NCDVGYGPQCQLVIOCEPLAEPLGTMDCTHPFGNFSFSSQCAFSCSEGTNLGTIEETT 240
QY 241 CGPFGMNSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTFICSEGTLLGKKK 300
Db 241 CGPFGMNSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTACTFICSEGTLLGKKK 300
QY 301 TICSSGIMNSPSPICQKLDKSFMSKIEGDYNDLPIPAVAVMTAFSGLAFTIWLARLKK 360
Db 301 TICSSGIMNSPSPICQKLDKSFMSKIEGDYNDLPIPAVAVMTAFSGLAFTIWLARLKK 360
QY 361 GKSKSRSMNDPY 372
Db 361 GKSKSRSMNDPY 372

RESULT 3
US-08-340-539A-2
; Sequence 2, Application US/08340539A
; Patent No. 5808025
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Kansas, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,539A
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gunnison, Jane
; REGISTRATION NUMBER: 38,479
; REFERENCE/DOCKET NUMBER: CG-104 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 385 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-340-539A-2

Query Match          98.1%; Score 2076; DB 1; Length 385;
Best Local Similarity 98.1%; Pred. No. 1.1e-181;
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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Db 74 YTDVAIONKAEIELEKTLFPSSRSYWIIGIRKIGIWTWGTNKSLEEAENMGDEPN 133  
QY 121 NKKNKEDCEVEIYIKRNKDGAKMNDACHKRLKAALCYTASCPWSCSGHGECEVEIINNHTC 180  
Db 134 NKKNKEDCEVEIYIKRNKDGAKMNDACHKRLKAALCYTASCPWSCSGHGECEVEIINNHTC 193  
QY 181 NCDVGYGPOQOLVIOCEPLAPELGTMDCTHPRGNFSSQCAFSCSEGTNLGIEETT 240  
Db 194 NCDVGYGPOQOLVIOCEPLAPELGTMDCTHPRGNFSSQCAFSCSEGTNLGIEETT 253  
QY 241 CGPFGNMSPEPTCOVIOCEPLAPDLGIMNC SHPLASFSTSACTFTCSGTELGKKK 300  
Db 254 CGPFGNMSPEPTCOVIOCEPLAPDLGIMNC SHPLASFSTSACTFTCSGTELGKKK 313  
QY 301 TICSSGIMSNPSPIQKRLDKSFSMIKEGDYNPLFIPAAVWTAFFSGLAFIIMLARLKK 360  
Db 314 TICSSGIMSNPSPIQKRLDKSFSMIKEGDYNPLFIPAAVWTAFFSGLAFIIMLARLKK 373  
QY 361 GKSKRSMDPY 372  
Db 374 GKSKRSMDPY 385

RESULT 4  
US-08-461-592B-2  
; Sequence 2, Application US/08461592B  
; Patent No. 5834425  
; GENERAL INFORMATION:  
; APPLICANT: Tedder, Thomas F.  
; APPLICANT: Kansas, Geoffrey S.  
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS  
; TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes  
; STREET: Ten Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,592B  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/340,539  
; FILING DATE: 16-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/008,459  
; FILING DATE: 25-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: CG-104  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 596-9000  
; TELEFAX: (212) 596-9090  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 385 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-461-592B-2

Query Match 98.1%; Score 2076; DB 2; Length 385;

Best Local similarity 98.1%; Pred. No. 1,1e-181;  
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MIFPWKCGSTQRDMLNTRKLMGWTMLCCDFLAHGTCTWTHYSEKPMNQARARFCNDN 60  
Db 14 MIFPWKCGSTQRDMLNTRKLMGWTMLCCDFLAHGTCTWTHYSEKPMNQARARFCNDN 73  
QY 61 YTDVAIONKAEIELEKTLFPSSRSYWIIGIRKIGIWTWGTNKSLEEAENMGDEPN 120  
Db 74 YTDVAIONKAEIELEKTLFPSSRSYWIIGIRKIGIWTWGTNKSLEEAENMGDEPN 133  
QY 121 NKKNKEDCEVEIYIKRNKDGAKMNDACHKRLKAALCYTASCPWSCSGHGECEVEIINNHTC 180  
Db 134 NKKNKEDCEVEIYIKRNKDGAKMNDACHKRLKAALCYTASCPWSCSGHGECEVEIINNHTC 193  
QY 181 NCDVGYGPOQOLVIOCEPLAPELGTMDCTHPRGNFSSQCAFSCSEGTNLGIEETT 240  
Db 194 NCDVGYGPOQOLVIOCEPLAPELGTMDCTHPRGNFSSQCAFSCSEGTNLGIEETT 253  
QY 241 CGPFGNMSPEPTCOVIOCEPLAPDLGIMNC SHPLASFSTSACTFTCSGTELGKKK 300  
Db 254 CGPFGNMSPEPTCOVIOCEPLAPDLGIMNC SHPLASFSTSACTFTCSGTELGKKK 313  
QY 301 TICSSGIMSNPSPIQKRLDKSFSMIKEGDYNPLFIPAAVWTAFFSGLAFIIMLARLKK 360  
Db 314 TICSSGIMSNPSPIQKRLDKSFSMIKEGDYNPLFIPAAVWTAFFSGLAFIIMLARLKK 373  
QY 361 GKSKRSMDPY 372  
Db 374 GKSKRSMDPY 385

RESULT 5  
US-08-513-278-4  
; Sequence 4, Application US/08513278  
; Patent No. 5840844  
; GENERAL INFORMATION:  
; APPLICANT: LASKY, LAURENCE A.  
; APPLICANT: STACHELL, SCOTT E.  
; APPLICANT: ROSEN, STEVEN D.  
; APPLICANT: SINGER, MARK S.  
; APPLICANT: YEDNOCK, TED A.  
; TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/513,278  
; FILING DATE: 10-AUG-1995  
; CLASSIFICATION: 5530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/059027  
; FILING DATE: 06-MAY-1993  
; APPLICATION NUMBER: 07/786149  
; FILING DATE: 31-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/315015  
; FILING DATE: 23-FEB-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Ginger R.  
; REGISTRATION NUMBER: 33,055  
; REFERENCE/DOCKET NUMBER: 565D1C1  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-3216  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 372 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-513-278-4

Query Match 78.0%: Score 1651; DB 2; Length 372;  
Best Local Similarity 76.1%: Pred. No. 6,3e-143;  
Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;

QY 1 MIFPMKQSTQRLDNIIFKLMGWTMLCCDFLAHNGTCWTYHSEKPMNMORARFCRDN 60  
DB 1 MIFPMKQSTQRLDNIIFKLMGWTMLCCDFLAHNGTCWTYHSEKPMNMENARKCKON 60  
QY 61 YTDLVAIONKKAIEYLELTKLPFSRSYWIIGIRKIGITWTWGTNKSITTEAENMGDEPN 120  
DB 61 YTDLVAIONKKAIEYLELTKLPFSRSYWIIGIRKIGITWTWGTNKSITTEAENMGDEPN 120  
QY 121 NKNKEDCCEIYIKRNDAGKMNDDACHKKAALCYTASQPSGSCGHGCEVEIINNHTC 180  
DB 121 NKNKEDCCEIYIKRNDAGKMNDDACHKKAALCYTASQPSGSCGHGCEVEIINNHTC 180  
QY 181 NCDVGYGPOQOLVIOCEPLAPELGTMDCHHPGNFSFSCAFSCSEGTNLGTLETT 240  
DB 181 NCDVGYGPOQOLVIOCEPLAPELGTMDCHHPGNFSFSCAFSCSEGTNLGTLETT 240  
QY 241 CGPFGNMSPEPTQVIOCEPLAPDLGIMNCSHPLASFTSACTFTICSEGTILGKKK 300  
DB 241 CGPFGNMSPEPTQVIOCEPLAPDLGIMNCSHPLASFTSACTFTICSEGTILGKKK 300  
QY 301 TICSSGSIWNSPICOQLKDSFSMIKEGDYNPFIPIVAVWTAFSGLAFTIWLARLKK 360  
DB 301 TICSSGSIWNSPICOQLKDSFSMIKEGDYNPFIPIVAVWTAFSGLAFTIWLARLKK 360  
QY 361 GKSKRSKMDPY 372  
DB 361 GKSKRSKMDPY 372

RESULT 6  
5514582-4  
PATENT NO. 5514582  
APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.  
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID  
IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 43  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/185,670  
FILING DATE: 21-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 986,931  
FILING DATE: 08-DEC-1992  
APPLICATION NUMBER: 808,122  
FILING DATE: 16-DEC-1991  
APPLICATION NUMBER: 440,625  
FILING DATE: 22-NOV-1989  
APPLICATION NUMBER: 315,015  
FILING DATE: 23-FEB-1989  
SEQ ID NO: 4  
LENGTH: 372  
5514582-4

Query Match 78.0%: Score 1651; DB 5; Length 372;  
Best Local Similarity 76.1%: Pred. No. 6,3e-143;  
Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;  
QY 1 MIFPMKQSTQRLDNIIFKLMGWTMLCCDFLAHNGTCWTYHSEKPMNMORARFCRDN 60

DB 1 MIFPMKQSTQRLDNIIFKLMGWTMLCCDFLAHNGTCWTYHSEKPMNMENARKCKON 60  
QY 61 YTDLVAIONKKAIEYLELTKLPFSRSYWIIGIRKIGITWTWGTNKSITTEAENMGDEPN 120  
DB 61 YTDLVAIONKKAIEYLELTKLPFSRSYWIIGIRKIGITWTWGTNKSITTEAENMGDEPN 120  
QY 121 NKNKEDCCEIYIKRNDAGKMNDDACHKKAALCYTASQPSGSCGHGCEVEIINNHTC 180  
DB 121 NKNKEDCCEIYIKRNDAGKMNDDACHKKAALCYTASQPSGSCGHGCEVEIINNHTC 180  
QY 181 NCDVGYGPOQOLVIOCEPLAPELGTMDCHHPGNFSFSCAFSCSEGTNLGTLETT 240  
DB 181 NCDVGYGPOQOLVIOCEPLAPELGTMDCHHPGNFSFSCAFSCSEGTNLGTLETT 240  
QY 241 CGPFGNMSPEPTQVIOCEPLAPDLGIMNCSHPLASFTSACTFTICSEGTILGKKK 300  
DB 241 CGPFGNMSPEPTQVIOCEPLAPDLGIMNCSHPLASFTSACTFTICSEGTILGKKK 300  
QY 301 TICSSGSIWNSPICOQLKDSFSMIKEGDYNPFIPIVAVWTAFSGLAFTIWLARLKK 360  
DB 301 TICSSGSIWNSPICOQLKDSFSMIKEGDYNPFIPIVAVWTAFSGLAFTIWLARLKK 360  
QY 361 GKSKRSKMDPY 372  
DB 361 GKSKRSKMDPY 372

RESULT 7  
US-08-110-158-4  
Sequence 4, Application US/08110158  
Patent No. 5605821  
GENERAL INFORMATION:  
APPLICANT: McEver, Rodger P.  
TITLE OF INVENTION: Expression Control Sequences of the  
TITLE OF INVENTION: P-Selectin Gene  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 1100 Peachtree Street, Suite 2800  
CITY: Atlanta  
STATE: GA  
COUNTRY: USA  
ZIP: 30309-4530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/110,158  
FILING DATE: 19930820  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/320,408  
FILING DATE: 08-MAR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-815-6558  
TELEFAX: (404)-815-6555  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 830 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-110-158-4







Best Local Similarity 36.1%; Pred. No. 1,9e-66;  
Matches 159; Conservative 55; Mismatches 109; Indels 117; Gaps 7;

QY	39	WTYHSKRPNNMORARFCRDNTYDLVAIONKAEIEYLEKTLPEFSKSYWIGIRKIGTW	98
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	23	WYSASTETWTFEDDAAYCOQRYTHLVAIONHAEIYELNSTFYSASYWIGIRKINGW	82
QY	99	TWYTKRSLTEEAENNGDEPPNNKKKECCVEIYIKRNKDAGKWDADCHKIKALCYTA	158
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	83	TWYGTKALPLETINNAPEBPNNKOSNECCVEIYIKRDNDSKWRDERSKKIKALCYTA	142
QY	159	SCQPMSCSGHGEVLEIINHTQNCIDGVGYPCQOLVIOCEPYLEAPELGIMDT	211
		:       :     :     :     :     :     :     :     :     :	
Db	143	ACTPTSCSGHGEIETINSTCQCYGRFGGLQCEQVVECDALFNLYNGVYTQPSLPMT	202
QY	212	-----HP-----FNGNS	218
		: : : : :     : : : : :     : : : : :     : : : : :	
Db	203	TAFECKEGFELIGEBHLQCTSSGSGWDKKPKCAKAVTCDTVGHPNQNDVSCNHSIGFEA	262
QY	219	FSSQAFCSGSEGTNLGTIGIBETTCGPGNMSSPEPKQVYICSEPLNAPRLGINCNH-FLA	277

Query Match 38.5%; Score 814.5; DB 2; Length 484;

TELEPHONE: (203) 776-1790  
TELEFAX: (203) 772-3655



.Sat, Jan 13 11:27:51 2001

us-09-119-209-2.raii

Page 9

? INFORMATION FOR SEQ ID NO: 9:  
 ? SEQUENCE CHARACTERISTICS:  
 ? LENGTH: 484 amino acids  
 ? TYPE: amino acid  
 ? STRANDEDNESS: Single  
 ? TOPOLOGY: Linear  
 ? MOLECULE TYPE: cDNA to mRNA  
 ? DESCRIPTION: predicted amino acid sequence of  
 ? DESCRIPTION: Porcine E-selectin  
 ? OS-09-276-197-9

Query Match	38.5%	Score 814.5	DB 3	Length 484
Best Local Similarity	36.1%	Pred. No. 1.9e-66		
Matches 159; Conservative	55;	Mismatches 109;	Indels 117;	Gaps 7;

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QY 39 WTTHYSEKPNWQRRARFCRDNYTDLVAIQNKAIEYLETLPFSSSYWIGIRKIGIM 98
      1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 23 WSYSAETETMTFDDASAYCQQRVTHLVAIQNHAIEIYLTSTFNYSASYWIGIRKINQTM 82

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QY 99 TWVGTSKSLTEEAENWGDGEPNNKKNKEDCVEIYIKRNKDAGKWNDDACHKLKALCYTA 158

Db 83 TWIGTKALLTPEATNMAPGEPNNKQSNEDCVEIYIKRDKDSGKWNDERCSKKKLLALCYTA 142

159 SCQPMSCSCHGECVEIINNHTCNCBVGYYGPQCQLVIOCEPLAEPLEGTMDCT----- 211

DB 143 ACTPTSCSGHGECEIETINNSIQCTPGFRGLQCEQVECDALENYNGVVICPQSLPMNT 202

**S**

27				EONES 2.1
28		:		

[illegible][illegible]

OV 278 SFSFTSACTFTCSGTEI.IGKKKTCSSGWSNPSPIC-----KIDKSFESMIRKED 330

Db 323 EFTYKSSCATSCCEEGFELRGSADLACTSOGOWTQEVPSQVYQCSSLFVYPREINMSCGE 3822

QY 331 YNPLF-----IPVAVMTA----- 344

Db 383 - - PVFGAVCTFACPEGWMNGSVALTCGATGHWGMLPTCEAPAESKIPLAMGLAAGVS 440

QY 345 -FSGLAFTIWLARRLKKGKK 363

Db 441 FMTSASELLWLLKRLRKRK 460

## RESULT 1.5

US-08-2/4-001B-38  
; Sequence 38, Application US/08274661B

FILING DATE: 13-JUL-1994  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/956701  
 FILING DATE: 10/01/1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dreger, Ginger R.  
 REGISTRATION NUMBER: 33,055  
 REFERENCE/DOCKET NUMBER: 761P1C10  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-3216  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 117 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear

Query Match	31.5%	Score	666	DB 1	Length	117			
Best Local Similarity	100.0%	Pred. No.	1	1e-53					
Matches	117	Conservative	0	Mismatches	0	Indels	0	Caps	0

QY	39	WTWYHSEKEMNNQRRARFECRDYWTYTLVAIQKAAELEYLEKTLPSRSRYWIGIRKIGGIM	98
Db	1	WTYHSEKPMNNQRRARFECRDYDTLVAIQKAAELEYLEKTLPSRSRYWIGIRKIGGIM	600
QY	99	TWVGTGKSLTEBERENWGDEPPNNKKNKEDCVETIYIKRNKDGAKKNDACRKLKLAALC	155
Db	61	TWVGTGKSLTEBERENWGDEPPNNKKNKEDCVETIYIKRNKDGAKKNDACRKLKLAALC	117

Search completed: January 13, 2001, 01:14:22  
Job time: 15633 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 13, 2001, 00:37:13 : Search time 127.23 Seconds  
(without alignments)  
427.383 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116  
Sequence: 1 MIFPMKOSTORDLMNIFKL.....WLARLKGKSKSRMNDPY 372

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 901307 seqs, 146172015 residues

Total number of hits satisfying chosen parameters: 901307

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Pending\_Patents\_MA:\*  
1: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep:\*  
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18: /cgn2\_6/ptodata/2/paa/US094\_COMB.pep:\*  
19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep:\*  
20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep:\*  
21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep:\*  
22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep:\*  
23: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
24: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
25: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
26: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
27: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
28: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2116	100.0	372	15	US-09-119-209-2
2	2076	98.1	385	1	PCT-US92-03970-2
3	2076	98.1	385	1	PCT-US94-00909-2
4	2076	98.1	385	4	US-08-008-459-2
5	2076	98.1	385	7	US-08-340-539-2

6	2076	98.1	385	8	US-08-410-569-2
7	1883	89.0	1078	22	US-60-212-659-523
8	1879	88.8	1078	22	US-60-207-315-428
9	1879	88.8	1078	22	US-60-230-435-1751
10	1651	78.0	372	15	US-09-119-209-4
11	905	42.8	830	1	PCT-US94-09395-4
12	905	42.8	830	1	US-08-449-687B-4
13	908	42.4	700	22	US-60-207-315-467
14	862	40.7	610	1	PCT-US99-28965-19
15	862	40.7	610	10	US-08-657-753-2
16	862	40.7	610	11	US-08-770-435-3
17	862	40.7	610	14	US-09-009-940A-89
18	666	31.5	119	22	US-60-160-203-6200
19	666	31.5	119	22	US-60-169-818-8687
20	645	30.5	119	22	US-60-169-867-5823
21	645	30.5	119	22	US-60-160-203-5003
22	586	27.7	116	22	US-60-169-840-6716
23	586	27.7	116	22	US-60-160-189-10011
24	586	27.7	116	22	US-60-160-203-6200
25	586	27.7	116	22	US-60-169-840-9326
26	452.5	21.4	129	22	US-60-169-867-7998
27	451.5	21.3	128	22	US-60-195-053-1909
28	451.5	21.3	129	22	US-60-195-053-1908
29	451.5	21.3	138	22	US-60-196-718-4238
30	447.5	21.1	133	22	US-60-196-718-4237
31	416	19.7	112	22	US-60-160-203-3503
32	415.5	19.6	130	22	US-60-196-718-903
33	415	19.6	134	22	US-60-192-739-3226
34	403	19.0	104	22	US-60-160-189-5792
35	389	18.4	115	22	US-60-196-718-3944
36	388	18.3	68	22	US-60-163-123-1859
37	388	18.3	68	22	US-60-163-123-1859
38	254	12.0	75	22	US-60-188-162-5010
39	247.5	11.7	135	22	US-60-196-718-4486
40	247.5	11.7	1124	22	US-60-191-637-1341
41	243.5	11.5	1124	22	US-60-191-681-1056
42	243.5	11.5	97	22	US-60-188-162-3972
43	243.5	11.5	101	22	US-60-188-162-3971
44	237	11.2	67	10	US-08-637-021A-8
45	236.5	11.2	86	22	US-60-196-174-862

#### ALIGNMENTS

RESULT 1  
US-09-119-209-2  
: Sequence 2, Application US/09119209  
: GENERAL INFORMATION:  
: APPLICANT: LASKY, LAURENCE A.  
: APPLICANT: STACHELL, SCOTT E.  
: APPLICANT: ROSEN, STEVEN D.  
: APPLICANT: SINGER, MARK S.  
: APPLICANT: YEDNOCK, TED A.  
: TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS  
: NUMBER OF SEQUENCES: 6  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Genentech, Inc.  
: STREET: 1 DNA Way  
: CITY: South San Francisco  
: STATE: California  
: COUNTRY: USA  
: ZIP: 94080  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: WinPatIn (Genentech)  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/119, 209  
: FILING DATE: 20-Jul-1998  
: CLASSIFICATION:  
: PRIOR APPLICATION DATA:

Sequence 2, Appl1
Sequence 523, App
Sequence 428, App
Sequence 1751, App
Sequence 4, Appl1
Sequence 4, Appl1
Sequence 467, App
Sequence 19, Appl1
Sequence 2, Appl1
Sequence 3, Appl1
Sequence 887, App
Sequence 868, App
Sequence 5823, App
Sequence 5003, App
Sequence 6716, App
Sequence 10011, A
Sequence 6200, App
Sequence 9326, App
Sequence 7998, App
Sequence 4236, App
Sequence 1909, App
Sequence 1908, App
Sequence 4238, App
Sequence 4237, App
Sequence 3503, App
Sequence 903, App
Sequence 3226, App
Sequence 5792, App
Sequence 3944, App
Sequence 1859, App
Sequence 4179, App
Sequence 5010, App
Sequence 4486, App
Sequence 1341, App
Sequence 1056, App
Sequence 3972, App
Sequence 3971, App
Sequence 862, App

APPLICATION NUMBER: 08/513278  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/059027  
FILING DATE: 6-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/786149  
FILING DATE: 31-OCT-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/315015  
FILING DATE: 23-FEB-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P0565D1C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 372 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
us-09-119-209-2

Query Match 100.0%; Score 2116; DB 15; Length 372;  
Best Local Similarity 100.0%; Pred. No. 7.2e-177;  
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDLNMIFKLMGWTMLCCDFLAHGGTCWTHYSEKPMWQARFRCDN 60  
DB 1 MIFPMKQSTORDLNMIFKLMGWTMLCCDFLAHGGTCWTHYSEKPMWQARFRCDN 60  
QY 61 YTDVAIQKAEIEYLEKTLPSRSYVWIGIRKIGIWTWGTNKSLEAEENMGDGEPN 120  
DB 61 YTDVAIQKAEIEYLEKTLPSRSYVWIGIRKIGIWTWGTNKSLEAEENMGDGEPN 120  
QY 121 NKKNEDECEIYIKRKNKAGKWNDACHKLKAALCYTASCPWSCSGHGECEVEIINNHTC 180  
DB 121 NKKNEDECEIYIKRKNKAGKWNDACHKLKAALCYTASCPWSCSGHGECEVEIINNHTC 180  
QY 181 NCDVGYGPOCOLVIOCEPLAEPELGTMDCTHPGPNFSSQCAFSCSEGTNLGIEETT 240  
DB 181 NCDVGYGPOCOLVIOCEPLAEPELGTMDCTHPGPNFSSQCAFSCSEGTNLGIEETT 240  
QY 241 CGPFGMWSSPEPTCOVIOCEPLADLGIMNCSHPLASFSTSACTFICSGTELLIGKKK 300  
DB 241 CGPFGMWSSPEPTCOVIOCEPLADLGIMNCSHPLASFSTSACTFICSGTELLIGKKK 300  
QY 301 TICSSGIGWSNPSPICKLDKSFMSIKREGDYNPLFIPIVAVWVTAFFSGLAFIWLARLKK 360  
DB 301 TICSSGIGWSNPSPICKLDKSFMSIKREGDYNPLFIPIVAVWVTAFFSGLAFIWLARLKK 360  
QY 361 GKSKRSNMNDPY 372  
DB 361 GKSKRSNMNDPY 372

RESULT 2

PCT-US92-03970-2

Sequence 2, Application PC/TUS9203970

GENERAL INFORMATION:

APPLICANT: Dana-Farber Cancer Institute, Inc.

TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED CELL SURFACE

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes

STREET: Ten Post Office Square

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US92/03970  
FILING DATE: 19920513  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Heine, Holliday C.  
REGISTRATION NUMBER: 34,346  
REFERENCE/DOCKET NUMBER: DECT-152Bq9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-2290  
TELEFAX: (617) 451-0313  
TELEX: 940675  
INFORMATION FOR SEQ. ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 385 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: Linear  
MOLECULE TYPE: protein  
PCT-US92-03970-2

Query Match 98.1%; Score 2076; DB 1; Length 385;  
Best Local Similarity 98.1%; Pred. No. 2.4e-173;  
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPMKQSTORDLNMIFKLMGWTMLCCDFLAHGGTCWTHYSEKPMWQARFRCDN 60  
DB 14 MIFPMKQSTORDLNMIFKLMGWTMLCCDFLAHGGTCWTHYSEKPMWQARFRCDN 73  
QY 61 YTDVAIQKAEIEYLEKTLPSRSYVWIGIRKIGIWTWGTNKSLEAEENMGDGEPN 120  
DB 74 YTDVAIQKAEIEYLEKTLPSRSYVWIGIRKIGIWTWGTNKSLEAEENMGDGEPN 133  
QY 121 NKKNEDECEIYIKRKNKAGKWNDACHKLKAALCYTASCPWSCSGHGECEVEIINNHTC 180  
DB 134 NKKNEDECEIYIKRKNKAGKWNDACHKLKAALCYTASCPWSCSGHGECEVEIINNHTC 193  
QY 181 NCDVGYGPOCOLVIOCEPLAEPELGTMDCTHPGPNFSSQCAFSCSEGTNLGIEETT 240  
DB 194 NCDVGYGPOCOLVIOCEPLAEPELGTMDCTHPGPNFSSQCAFSCSEGTNLGIEETT 253  
QY 241 CGPFGMWSSPEPTCOVIOCEPLADLGIMNCSHPLASFSTSACTFICSGTELLIGKKK 300  
DB 254 CGPFGMWSSPEPTCOVIOCEPLADLGIMNCSHPLASFSTSACTFICSGTELLIGKKK 313  
QY 301 TICSSGIGWSNPSPICKLDKSFMSIKREGDYNPLFIPIVAVWVTAFFSGLAFIWLARLKK 360  
DB 314 TICSSGIGWSNPSPICKLDKSFMSIKREGDYNPLFIPIVAVWVTAFFSGLAFIWLARLKK 373  
QY 361 GKSKRSNMNDPY 372  
DB 374 GKSKRSNMNDPY 385

RESULT 3

PCT-US94-00909-2

Sequence 2, Application PC/TUS9400909

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: CHIMERIC SELECTINS AS STIMULANEOUS BLOCKING

TITLE OF INVENTION: AGENTS FOR COMPONENT SELECTIN FUNCTION

NUMBER OF SEQUENCES: 11

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: PCT/US94/00909
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: US 08/008,459
5 FILING DATE: 25-JAN-1993
6 PRIOR APPLICATION DATA:
7 APPLICATION NUMBER: US 07/983,606
8 FILING DATE: 30-NOV-1992
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: US 07/962,483
11 FILING DATE: 02-APR-1992
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 07/770,608
14 FILING DATE: 03-OCT-1991
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 07/737,092
17 FILING DATE: 29-JUL-1991
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 07/730,503
20 FILING DATE: 08-JUL-1991
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 07/700,773
23 FILING DATE: 15-MAY-1991
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/313,109
26 FILING DATE: 21-FEB-1989
27 INFORMATION FOR SEQ ID NO: 2:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 385 amino acids
30 TYPE: amino acid
31 TOPOLOGY: linear
32 MOLECULE TYPE: protein
33 PCT-US94-00909-2

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Query Match	98.1%	Score 2076	DB 1	Length 385
Best Local Similarly	98.1%	Pred. No. 2.4e-173		
Matches 365	Conservative 3	Mismatches 4	Indels 0	Gaps 0

QY	1	MIFPMKCSQTRDLAMNIFKLMGWMLCCDFLAHHGTCWTHVSEKPMNQARRECRDN	60
Db	14	MIFPMKCSQTRDLAMNIFKLMGWMLCCDFLAHHGTCWTHVSEKPMNQARRECRDN	73
QY	61	YTDLVAIQNKAIELEYLEKTLPEFSRSYWIIGIRKIGGIWTVGNTKSLTEAEWNGDSEPN	120
Db	74	YTDLVAIQNKAIELEYLEKTLPEFSRSYWIIGIRKIGGIWTVGNTKSLTEAEWNGDSEPN	133
QY	121	NKKKKEDCEVEYIRKRNKDAGKMNDDACHKLLKALCTYASQPMSCSHGECVEIINNHTC	180
Db	134	NKKKKEDCEVEYIRKRNKDAGKMNDDACHKLLKALCTYASQPMSCSHGECVEIINNYTC	193
QY	181	NCDDVGYGPOOLYIOCEBLEAPLGTMDCHNPGNFSFSSQCAFSCSEGTNLTGIEETT	240
Db	194	NCDDVGYGPOOLYIOCEBLEAPLGTMDCHNPGNFSFSSQCAFSCSEGTNLTGIEETT	253
QY	241	CGPFGNMSPEPTQVIOCEPLASAPDLGIMNCSHPPLASFSTSACTEICSEGTELLKRR	300
Db	254	CGPFGNMSPEPTQVIOCEPLASAPDLGIMNCSHPPLASFSTSACTEICSEGTELLKRR	313
QY	301	TICSSGIGWSNPDIQCKLDKSFSSMIKEGDYNPLFIPAAVMTAFSGIAFIIMLARLKK	360
Db	314	TICSSGIGWSNPDIQCKLDKSFSSMIKEGDYNPLFIPAAVMTAFSGIAFIIMLARLKK	373
QY	361	GKKSKRSMDPY 372	
Db	374	GKKSKRSMDPY 385	

RESULT 4  
US-08-008-459-2  
; Sequence 2, Application US/08008459  
; GENERAL INFORMATION:  
; APPLICANT: Tedder, Thomas F.

```

1 APPLICANT: Kansas, Geoffrey S.
2 TITLE OF INVENTION: CHEMICE SELECTINS AS SIMULTANEOUS
3 TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
4 NUMBER OF SEQUENCES: 11
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
7 STREET: Ten Post Office Square
8 CITY: Boston
9 STATE: MA
10 COUNTRY: USA
11 ZIP: 02109
12
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent In Release #1.0, Version #1.25
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/008,459
20 FILING DATE: 25-JAN-1993
21 CLASSIFICATION: 514
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 07/983,606
24 FILING DATE: 30-NOV-1992
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 07/862,483
27 FILING DATE: 02-APR-1992
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 07/770,608
30 FILING DATE: 03-OCT-1991
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 07/737,092
33 FILING DATE: 29-JUL-1991
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 07/730,503
36 FILING DATE: 08-JUL-1991
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 07/700,773
39 FILING DATE: 15-MAY-1991
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 07/313,109
42 FILING DATE: 21-FEB-1989
43 ATTORNEY/AGENT INFORMATION:
44 NAME: Helne, Holliday C.
45 REGISTRATION NUMBER: 34,346
46 REFERENCE/DOCKET NUMBER: DPCI-318XX
47 TELECOMMUNICATION INFORMATION:
48 TELEPHONE: (617) 542-2290
49 TELEFAX: (617) 451-0313
50 TELEX: 940675
51 INFORMATION FOR SEQ ID NO: 2:
52 SEQUENCE CHARACTERISTICS:
53 LENGTH: 385 amino acids
54 TYPE: amino acid
55 TOPOLOGY: linear
56 MOLECULE TYPE: protein
57
58 US-08-008-459-2

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Query Match	98.1%;	Score 2076;	DB 4;	length 385;
Best Local Similarity	98.1%;	Pred. No. 2.4e-173;		
Matches 365;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0

Qy	1	MIFPMKCSOTRDLMNFEFLKMGMTMLCCDFLAHHGYICWYHYHSEKPMNQARARFCRD	60
Db	14	MIFPMKCSOTRDLMNFEFLKMGMTMLCCDFLAHHGYICWYHYHSEKPMNQARARFCRD	73
Qy	61	YTTDLVALONKAEIYLEKTPDFSRSSYWIIGIRKGGIWTWYGVTKSKLSTEEAENMGDEPN	120
Db	74	YTTDLVALONKAEIYLEKTPDFSRSSYWIIGIRKGGIWTWYGVTKSKLSTEEAENMGDEPN	133
Qy	121	NKKNKEDCEVELYIKRNKDAGKMNDDACHKLAAALCYTASCPWMSGSHGECVELIINHTC	180
Db	134	NKKNKEDCEVELYIKRNKDAGKMNDDACHKLAAALCYTASCPWMSGSHGECVELIINHTC	193

```

? TELEFAX: (617) 451-0313
? TELEX: 940675
? INFORMATION FOR SEQ. ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 385 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? OS-08-340-539-2

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Query Match	98.1%;	Score 2076;	DB 7;	Length 385;
Best Local Similarity	98.1%;	Pred. No. 2.4e-173;		
Matches 365;	Conservative	3;	Mismatches 4;	Indels 0;
			Gaps	0;

conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 MIEPWKCOSTORDLWNI EKLWGWTMLCCDEFLAHGTYCWTYHYSEKPMNWQARARECRDN 60

61 YTDVAIQNAEIEYLEKTPFSRSYYWIGIRKIGGIWTVGTINKSLTEEAENWGDEPN 120

74 VENTIVATORUM ET ALIIUM 120

14 IDLVAILQNNAEILEYLEKTLPPFSRSYYWIGIRKIGGIWTVGNTNKSLSLEEAEENWGDGEPN 133

QY 121 NKKNKEDCVEIYIKRNKDAGKWNDDACHKLKALCYTASCQPWSCSGHGCEVEIINNHTC 180

Db 134 NKKNKEDVEIYIKRNDAGKWNDDACHIKALCYTASCPWSCSCSCGEVETIIVVTC 103

181 NCDVGVVCPDGGCVTIOGCVFV... 193

[illegible]

Db 194 NCDVGYGPGCCQFVIOCEPLEAPELGTMDCTHPLGNFNFNNSQCAFSCSEGTNLGIEET 253

QY 241 CGPFGNWSSEPTCQVIOCEPLSAPDLGIMNCSHPLASFSTACTFTICSECTETIVVV 300

[illegible]

CELLONMSOFFEICQVIOCEPLSAPDLGIMNCSHPLASFSTFACTFICSEGTELIGKK 313

301 TICSSSGIWSNPSPICQKLDKSFMSIKEGDYNPLFIPVAVMTAFSGLAFI IWLARRLK 360

Db 314 TICESSGIWSNPSPICQKLDKSFMSIKEGDYNPLFIPVAVMYTAFSGIAFTIWTABPIK 373

361 GKKSKRSMNDPY 372

**A**

3/4 GKSSKRSMNDPY 385

RESULT 6  
JS-08-410-569-2

Sequence 2, Application US/08410569

GENERAL INFORMATION:  
APPLICANT: Tedder Thomas F

APPLICANT: Spertini, Olivier G.

TITLE OF INVENTION: LEUKOCYTE ADHESION MOLECULE-1 (LAM-1)  
TITLE OF INVENTION: AND LIGAND THEREOF

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Weidarten Schurja GmbH  
Weidarten Schurja GmbH

STREET: Ten Post Office Square

CITY: Boston  
STATE: MA

COUNTRY: USA  
ETD 00100

ZIP: 02109  
COMPUTER READABLE FORM.

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/410 560

FILING DATE: 08/08/2009

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/770,608

FILING DATE: 03-OCT-1991  
APPLICATION NUMBER: US 07/700 773

**Figure 1**

FILING DATE: 15-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Heine, Holliday C.  
REGISTRATION NUMBER: 34,346  
REFERENCE/DOCKET NUMBER: DFCG-152EX  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-2290  
TELEFAX: (617) 451-0313  
TELEX: 940675  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 385 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-410-569-2

Query Match 98.1%; Score 2076; DB 8; Length 385;  
Best Local Similarity 98.1%; Pred. No. 2.4e-173;  
Matches 365; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MIFPKCSTORDLWIKKLMGWTMLCCDPLAHGCTYTHYSEKPMNMORARFCNDN 60  
DB 14 MIFPKCSTORDLWIKKLMGWTMLCCDPLAHGCTYTHYSEKPMNMORARFCNDN 73  
QY 61 YTDVAIONKAEIEYLEKTLPPSRSYWIGIRKIGITWVGTNKSLEEAENMGDEPN 120  
DB 74 YTDVAIONKAEIEYLEKTLPPSRSYWIGIRKIGITWVGTNKSLEEAENMGDEPN 133  
QY 121 NKKNKEDVEIYIKRNKDGAKMNDACHKLAALCYTASCPWMSGSGHECEIINNHTC 180  
DB 134 NKKNKEDVEIYIKRNKDGAKMNDACHKLAALCYTASCPWMSGSGHECEIINNHTC 193  
QY 181 NCDVGYTPQCQLVYQCEPLAEPLGTMDCTHPGNSFSFSCAFSGEGNLTGIEETT 240  
DB 194 NCDVGYTPQCQLVYQCEPLAEPLGTMDCTHPGNSFSFSCAFSGEGNLTGIEETT 253  
QY 241 CGPGNMSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTFSACTFICSEGTELIGKK 300  
DB 254 CGPGNMSSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSTFSACTFICSEGTELIGKK 313  
QY 301 TICSSGIMNSPPIQCKLDSFMSIKEDYNPFIPIVAVWVTAESGLAFIIMLARLKK 360  
DB 314 TICSSGIMNSPPIQCKLDSFMSIKEDYNPFIPIVAVWVTAESGLAFIIMLARLKK 373  
QY 361 GKSKRSNDPY 372  
DB 374 GKSKRSNDPY 385

RESULT 7  
US-60-212-659-523  
Sequence 523, Application US/60212659  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CL000674  
CURRENT APPLICATION NUMBER: US/60/212,659  
CURRENT FILING DATE: 2000-06-19  
NUMBER OF SEQ ID NOS: 879  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 523  
LENGTH: 1078  
TYPE: PRT  
ORGANISM: HUMAN  
US-60-212-659-523

Query Match 89.0%; Score 1883; DB 22; Length 1078;  
Best Local Similarity 97.4%; Pred. No. 6.5e-156;

Matches 336; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 22 GWTMLCCDPLAHGCTYTHYSEKPMNMORARFCNDVYTDVAIONKAEIEYLEKTL 81  
DB 604 GYFLPSKDFLAHGTDCWTHYSEKPMNMORARFCNDVYTDVAIONKAEIEYLEKTL 663  
QY 82 FRSRYTWIGIRKIGITWVGTNKSLEEAENMGDEPNKKKEDCEIYIKRNKDGAK 141  
DB 664 FRSRYTWIGIRKIGITWVGTNKSLEEAENMGDEPNKKKEDCEIYIKRNKDGAK 723  
QY 142 WNDACCHKLAALCYTASCPWMSGSGHECEIINNHTCNCDVGYGQCQLVIOCEPLE 201  
DB 724 WNDACCHKLAALCYTASCPWMSGSGHECEIINNHTCNCDVGYGQCQLVIOCEPLE 783  
QY 202 APELCTMDCTHPGNSFSFSCAFSGEGNLTGIEETTCCPGFNMSSPEPTCOVIOCEP 261  
DB 784 APELCTMDCTHPGNSFSFSCAFSGEGNLTGIEETTCCPGFNMSSPEPTCOVIOCEP 843  
QY 262 LSAPDLGIMNCSHPLASFSTFSACTFICSEGTELIGKKKTICSSGIMNSPPIQCKL 321  
DB 844 LSAPDLGIMNCSHPLASFSTFSACTFICSEGTELIGKKKTICSSGIMNSPPIQCKL 903  
QY 322 SFSMIKEDYNPFIPIVAVWVTAESGLAFIIMLARLKKKKSKR 366  
DB 904 SFSMIKEDYNPFIPIVAVWVTAESGLAFIIMLARLKKKKSKR 948

RESULT 8  
US-60-207-315-428  
Sequence 428, Application US/60207315  
GENERAL INFORMATION:  
APPLICANT: Beasley, Ellen  
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,  
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: CL000601  
CURRENT APPLICATION NUMBER: US/60/207,315  
CURRENT FILING DATE: 2000-05-30  
NUMBER OF SEQ ID NOS: 528  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 428  
LENGTH: 1078  
TYPE: PRT  
ORGANISM: HUMAN  
US-60-207-315-428

Query Match 88.8%; Score 1879; DB 22; Length 1078;  
Best Local Similarity 97.1%; Pred. No. 1.4e-155;  
Matches 335; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 22 GWTMLCCDPLAHGCTYTHYSEKPMNMORARFCNDVYTDVAIONKAEIEYLEKTL 81  
DB 604 GYFLPSKDFLAHGTDCWTHYSEKPMNMORARFCNDVYTDVAIONKAEIEYLEKTL 663  
QY 82 FRSRYTWIGIRKIGITWVGTNKSLEEAENMGDEPNKKKEDCEIYIKRNKDGAK 141  
DB 664 FRSRYTWIGIRKIGITWVGTNKSLEEAENMGDEPNKKKEDCEIYIKRNKDGAK 723  
QY 142 WNDACCHKLAALCYTASCPWMSGSGHECEIINNHTCNCDVGYGQCQLVIOCEPLE 201  
DB 724 WNDACCHKLAALCYTASCPWMSGSGHECEIINNHTCNCDVGYGQCQLVIOCEPLE 783  
QY 202 APELCTMDCTHPGNSFSFSCAFSGEGNLTGIEETTCCPGFNMSSPEPTCOVIOCEP 261  
DB 784 APELCTMDCTHPGNSFSFSCAFSGEGNLTGIEETTCCPGFNMSSPEPTCOVIOCEP 843  
QY 262 LSAPDLGIMNCSHPLASFSTFSACTFICSEGTELIGKKKTICSSGIMNSPPIQCKL 321  
DB 844 LSAPDLGIMNCSHPLASFSTFSACTFICSEGTELIGKKKTICSSGIMNSPPIQCKL 903  
QY 322 SFSMIKEDYNPFIPIVAVWVTAESGLAFIIMLARLKKKKSKR 366  
DB 904 SFSMIKEDYNPFIPIVAVWVTAESGLAFIIMLARLKKKKSKR 948

Db 904 SFSMIKEDGYNPLFIPIVAVMTAFSGLAFLIIMLARLKKGKSKR 948

RESULT 9

US-60-230-435-1751

Sequence 1751, Application US/60230435

GENERAL INFORMATION:

APPLICANT: Beasley, Ellen

TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: C1000768

CURRENT APPLICATION NUMBER: US/60/230,435

CURRENT FILING DATE: 2000-09-06

NUMBER OF SEQ ID NOS: 2991

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO: 1751

LENGTH: 1078

TYPE: PRT

ORGANISM: HUMAN

US-60-230-435-1751

Query Match 88.8%; Score 1879; DB 22; Length 1078;

Best Local Similarity 97.1%; Pred. No. 1,4e-155;

Matches 335; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 22 GWTMLCDPFLAHGTYCTHYHSEKPMNMOARRCRNITDVAIQKAEIYELEKTL 81

Db 604 GYFLSPKDFLAHGHGTDCWTHYSEKPMNMOARRCRNITDVAIQKAEIYELEKTL 663

QY 82 FRSRYWYGIKRIKIGIWTWGTNKSLEAEENWGDEPNKKKNEDEVEIYIKRNKDAK 141

Db 664 FRSRYWYGIKRIKIGIWTWGTNKSLEAEENWGDEPNKKKNEDEVEIYIKRNKDAK 723

QY 142 WNDACHLKAALCYTASCPMSCSGHGECEVEIINNHTCNDVYGGQCOLVIOCEPLE 201

Db 724 WNDACHLKAALCYTASCPMSCSGHGECEVEIINNHTCNDVYGGQCOLVIOCEPLE 783

QY 202 APELGTMDCTHPFGNFSFSSQAFSCSEGTNLGIEETTCGPFGNWSSPEPTCOVIOCEP 261

Db 784 APELGTMDCTHPFGNFSFSSQAFSCSEGTNLGIEETTCGPFGNWSSPEPTCOVIOCEP 843

QY 262 LSAADLGIMNCSHPLASFTSACTFICSEGTELIGKKTICSSGSIWNSPICOQLDK 321

Db 844 LSAADLGIMNCSHPLASFTSACTFICSEGTELIGKKTICSSGSIWNSPICOQLDK 903

QY 322 SFSMIKEDGYNPLFIPIVAVMTAFSGLAFLIIMLARLKKGKSKR 366

Db 904 SFSMIKEDGYNPLFIPIVAVMTAFSGLAFLIIMLARLKKGKSKR 948

RESULT 10

US-09-119-209-4

Sequence 4, Application US/09119209

GENERAL INFORMATION:

APPLICANT: LASKY, LAURENCE A.

APPLICANT: STACHELL, SCOTT E.

APPLICANT: ROSEN, STEVEN D.

APPLICANT: SINGER, MARK S.

APPLICANT: YEDNOCK, TED A.

TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/119,209

FILING DATE: 20-Jul-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/513278

FILING DATE: 10-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/059027

FILING DATE: 6-MAY-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/786149

FILING DATE: 31-OCT-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/315015

FILING DATE: 23-FEB-1989

ATTORNEY/AGENT INFORMATION:

NAME: Love, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P0565D1C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5530

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 372 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-09-119-209-4

Query Match 78.0%; Score 1651; DB 15; Length 372;

Best Local Similarity 76.1%; Pred. No. 3.6e-136;

Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;

QY 1 MIPPMKQSTQFORDIMNIFKLMGWTMLCDPFLAHGTYCTHYHSEKPMNMOARRCFCDN 60

Db 1 MVEPMKEGTWYMSRNILKLMWTLCCPFLHGHGTWTHYSEKPMNMOARRCFCDN 60

QY 61 YTDVAIQKAEIYELEKTLFPRSRYWYGIKRIKIGIWTWGTNKSLEAEENWGDEPN 120

Db 61 YTDVAIQKAEIYELEKTLFPRSRYWYGIKRIKIGIWTWGTNKSLEAEENWGDEPN 120

QY 121 NKNKNEDEVEIYIKRNKDAKGNNDACHLKAALCYTASCPMSCSGHGECEVEIINNHTC 180

Db 121 NKNKNEDEVEIYIKRNKDAKGNNDACHLKAALCYTASCPMSCSGHGECEVEIINNHTC 180

QY 181 NCDVYGGQCOLVIOCEPLEAPELGTMDCTHPFGNFSFSSQAFSCSEGTNLGIEETT 240

Db 181 ICDAGYGGQCYVVOCEPLEAPELGTMDCTHPFGNFSFSSQAFSCSEGTNLGIEETT 240

QY 241 CGPFGNWSPEPTCOVIOCEPLASADLGIMNCSHPLASFTSACTFICSEGTELIGKR 300

Db 241 CGASGNWSSPEPTCOVIOCEPLASADLGIMNCSHPLASFTSACTFICSEGTELIGKR 300

QY 301 TICSSGSIWNSPICOQLDKSFSMIKEDGYNPLFIPIVAVMTAFSGLAFLIIMLARLKK 360

Db 301 TCGASGNWSSPEPTCOVIOCEPLASADLGIMNCSHPLASFTSACTFICSEGTELIGKR 360

QY 361 GKSKRSRNDPY 372

Db 361 GKSKRSRMDPY 372

RESULT 11

PCT-US94-09395-4

Sequence 4, Application PC/TUS9409395

GENERAL INFORMATION:

APPLICANT: Board of Regents of the University of Oklahoma

TITLE OF INVENTION: Expression Control Sequences of the P-Selectin Gene

NUMBER OF SEQUENCES: 17



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-4530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER:
APPLICATION NUMBER: PCT/US94/09395
FILING DATE: 19-AUG-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 830 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-09395-4

```

Query Match	42.88;	Score 905;	DB 1;	Length 830;
Best Local Similarity	50.68;	Pred. No. 1.9e-70;		
Matches 157; Conservative	47;	Mismatches 106;	Indels 0;	Gaps 0

Qy	8	QSTORDLMNIEKRLGWMMLCCDFLAHNGTCVTHYHSEKPNMNOBARPCRDYTDVAI	67
Dd	11	QRFRVAVFGISOLLCCFSAIISSELTNOKEVAAWMTYHSTKAVSNMUISKRYQONKRTDLVAI	70
Qy	68	QNKKEIYLEKTLTLPFSNYSYWTGTRKGGTWTYVGTNKSILTBEANNGDCEPNNKKKED	127
Dd	71	QNKNEIDYLNKVLTYESSYTWIGTRKNKKTKWTWTGTRKALTNEANMADNEPNNKRNED	130
Qy	128	CVETIYIRKKNKDGKMNDDACHKLEALACTYASCOPMSCSGHCEVETIINNHTCNCIDGYV	187
Dd	131	CVETIYIKSPARKMNDENHCKKKKHALCTYASCODMCSNQGDELTICWYTCSCTGCFY	190
Qy	188	GPQCQVLYIOCEPRLAPBLGTMDCTHPRGNFSFSQCAFSCSEGTNLTGLIETTCGPPGNM	247
Dd	191	GPCEEVYREGCELTLPQHVLMNCNSHPRGNFSFSQCSFCFTDGYQVNGPSKLCCLASGIW	250
Qy	248	SSPEPTCOVIOCEPRLAPADLGIMNCSHPRLASFSTSACTFICSBGRLTICKKRTICSSG	307
Dd	251	TNKRPGCLANQCPRLKTRPGRNMICLHSAKAFQHOSSCSFCEBGRFALVDEPYVQCTASG	310
Qy	308	TWSNPSPTCO 317	
Dd	311	VWTPAPAPVCK 320	

RESULT 12  
US-08-449-687B-4  
Sequence 4, Application US/08449687B  
GENERAL INFORMATION:  
APPLICANT: MCEVER, Rodger P.  
APPLICANT: Pan, Junliang  
TITLE OF INVENTION: Expression Control sequences of the  
TITLE OF INVENTION: P-Selectin Gene  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patricia L. Pabst  
STREET: 2800 One Atlantic Center

STREET: 1201 West Peachtree Street  
 CITY: Atlanta  
 STATE: GA  
 COUNTRY: USA  
 ZIP: 30309-3450  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, V  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/449,687B  
 FILING DATE: 24-MAY-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/110,158  
 FILING DATE: 20-AUG-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/320,408  
 FILING DATE: 08-MAR-1989  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patricia L.  
 REGISTRATION NUMBER: 31,284  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (404)873-8794  
 TELEFAX: (404)873-8795  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 830 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 OS-08-449-687b-4

US-08-449-687B-4

Query Match	42.8%	Score 905	DB 8	Length 830	
Best Local Similarity	50.6%	Pred. No. 1.9e-70			
Matches 157	Conservative 47	Mismatches 106	Indels 0	Gaps 0	
QY	8	OSTORDLMNIRKLMGWTMLCCDFLAHGHGTCYWTYHSEKPMNMQARAPRCRDNYTDLVAI	67		
Db	11	QRFQGVVVGISQLLCEFSALLISELTNQKEVAAMTYHSTKAVSMNLSRKKCQARRYTDVAI	70		
QY	68	QNKAEILELEKTLTPSPRSYTWIGIRK ICGIMTWGVTNKS LTIIEAENMGDGEPRNKKKED	127		
Db	71	QNKNEIDYLVNKLVPYSSSYTWIGIRKNNKTWTWGTAKALTNEAENMADNEPNRNNKED	130		
QY	128	CVEYIIRKNKNDGAKNNDDACHKIKALKALCYTASCPWMSGSGHECEYIINNHKNCNDVGY	187		
Db	131	CVEYIIRKSPSAPAGKNNDDHCLKIKKHALCYTASCPWMSGSGHECEYIIGNYVSCYPCFY	190		
QY	188	GPQCOLVIOCEPLAEPLDELGTMDCTHPFCNFSFSSOCAPSCSEGTMLTGJIEETTCGPPGM	247		
Db	191	GPECEYVAGCEBELPQHVLMNKNCHPLOSFNSSQCSFHCITDGYQVNGPSKIECLASGIV	250		
QY	248	SSPEPTCOVIOCEPLASAPDLGIMNCSHPILASTFSPTSACTFLICSEGTELLGKKKTICESSG	307		
Db	251	TNKPPOCIACACCPPLKIPERGNCMLTCHSAKAFHOHSSCSFSCCEGCFALVGPVEVQCTASG	310		
QY	308	ITWSNDSPICQ	317		
Db	311	VMTAPAPVCK	320		

```

RESULT 13
US-60-207-315-467
; Sequence 467, Application US/60207315
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEIN,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF

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Page 8

QY 39 WTYYHSEKEMNORARFECRDNYDTLVAIONKAIEYLEXTLPFSRYTWIGIRKGIM 98  
I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :  
Db 22 WMINSTEAMTYDEASAYCQQRITHLAIVIONKEEIEYLSITSYSBYWIGIRKVNVW 81  
QY 99 TWTGWNKSLTEAEANWGCEENNNKKNEEDVELITYRNKDACKWMDACIKAKALCYTA 158

**D**b    142 ACGTTCSCGSHGCVELINNYTKCRDPEFSGLKEQIVNCTALESPEHOSILVCSHPLEFGS 2015

OY 219 FSSQCAFSCSEGTNLTGIEFTTCGPEGNWSSPEPTCOVIOCEPLSAPDGLIMNCSPILAS 278  
Db 202 YNSSCSISCDRGLPSSMETMQCMSSGEMSAPIPACNVECDVATNPANGFVECFQNPQS 261  
OY 279 FSTISACTFICSEGTGELGKKKTICSSSGIWSNPSPICQ 317  
Db 262 FPMNTTCTTFDECEGFELMGAOSLOCTSSGNMNDNEKPTCK 300

Search completed: January 13, 2001, 01:56:54  
Job time: 4781 sec

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OM of: US-09-119-209-2 to: GenBank: \* out-format: pfs

Date: Jan 13, 2001 3:07 AM

About: Results were produced by the GenCore software, version 4.5.  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-MODEL=firmer-p2n.model -DEV=xlp
-O/cgcn2.1/USPTO.spool/US09119209/runal.08012001.083824.1922/app-query.fasta.1.434
-DB=GenBank -OFMT=fasta -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEX=7.000 -START=1 -MATRIX=blonum62 -TRANS=human40.cd1
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTPMT=pfs -NORMEXT -MINLEN=0
-MAXLEN=200000000 -USER=US09119209/cgcn1_1.4795 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPHY -WAIT -THREADS=1
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Search Information block:

Query: US-09-119-209-2

Query length: 372

Database: GenBank: \*

Database sequences: 1118133

Database length: -1736092196

Search time (sec): 1246.430000

score\_list:

Sequence	Strd Orig	%score	EScore	Len	Documentation
gb_pat1:AR060685	+ 2116.00	3320.29	8.7e-177	2259	AR060685 Sequence 1 from patent
gb_pat1:MMPLNHR	+ 2110.00	3310.82	2.9e-175	2259	X16070 Human mRNA for p1n hom
gb_pat1:HUMLNHR	+ 2094.00	3285.19	7.9e-175	2354	M2580 Human lymph node homing
gb_pat1:USA246000	+ 2090.00	3282.49	1.1e-174	1569	AJ246000 Homo sapiens mRNA for
gb_pat1:PTU37328	+ 2085.00	3277.62	2.1e-174	1119	U73728 Pan troglodytes L-select
gb_pat1:ISLEUB	+ 2082.00	3266.37	8.8e-174	2323	X16150 Human mRNA for leu-8 p
gb_pat1:ISLEYAM1	+ 2076.00	3256.87	3.0e-173	2330	X16150 Human lymph node homing
gb_pat1:AR016679	+ 2076.00	3256.87	3.0e-173	2330	AR016679 Sequence 1 from patent
gb_pat1:AR040718	+ 2076.00	3256.87	3.0e-173	2330	AR040718 Sequence 1 from patent
gb_pat1:AR054061	+ 2076.00	3256.87	3.0e-173	2330	AR054061 Sequence 1 from patent
gb_pat1:IT70140	+ 2076.00	3256.87	3.0e-173	2330	IT70140 Sequence 1 from patent
gb_pat1:PPU73729	+ 2062.00	3241.31	2.2e-172	1119	U73729 Pongo pygmaeus L-select
gb_pat1:IMU073704	+ 1996.00	3137.12	1.4e-166	1510	U52074 Macaca mulatta L-select
gb_pat1:PHU52074	+ 1992.00	3128.13	4.4e-166	1510	U52074 Macaca mulatta L-select
gb_pat1:OCU26535	+ 1796.00	2817.77	8.6e-149	1680	U26535 Oryctolagus cuniculus I
gb_pat1:BTLECAM1	+ 1695.00	2653.06	9.9e-140	2650	X62882 B. taurus mRNA for LECAM
gb_pat1:ST9523	+ 1667.00	2614.68	1.8e-137	1580	S79523 lymphocyte membrane p
gb_pat1:RATLECAM1	+ 1653.00	2594.51	2.3e-136	1272	D10831 Rat mRNA for LECAM-1, c
gb_pat1:MUSLECAM1	+ 1651.00	2590.30	4.0e-136	1431	M36005 Mouse lymph node homing
gb_pat1:MUSMLHR	+ 1651.00	2590.30	4.0e-136	1431	M36058 Mouse lymph node homing
gb_pat1:MUSLHR	+ 1651.00	2590.01	4.2e-136	1479	X14772 Mouse mRNA for lymph n
gb_pat1:MUSLHR	+ 1651.00	2586.47	6.5e-136	2199	M23322 Mouse mRNA for lymph n
gb_pat1:AR060686	+ 1651.00	2586.41	6.6e-136	2214	AR060686 Sequence 3 from patent
gb_pat1:MUSLHR2	+ 933.00	1445.57	2.3e-72	5076	M64545 Sequence 2 from patent
gb_pat1:SHPE	+ 920.00	1431.12	1.5e-71	2569	L34270 Ovis aries (clone 12) B
gb_pat1:IT36305	+ 905.00	1405.65	3.9e-70	3142	I36305 Sequence 3 from patent
gb_pat1:HUMGMP140	+ 903.00	1405.65	3.9e-70	3142	M23322 Human granule membrane
gb_pat1:MUSGMP140A	+ 902.50	1403.53	5.1e-70	2558	M73732 Mus musculus granulose me
gb_pat1:MUSSELEC	+ 902.50	1401.89	6.3e-70	3075	M87861 Mus musculus P-selectin
gb_pat1:BOVSELEC	+ 894.50	1390.41	2.7e-69	2703	L12041 Bovine P-selectin mRNA
gb_pat1:BOVSELEC	+ 885.00	1373.95	2.3e-68	3185	L23088 Rattus norvegicus P-se
gb_pat1:DOGMPL10A	+ 884.00	1374.93	2.0e-68	2391	M88170 Canis familiaris cell a
gb_pat1:PIGSELE	+ 878.50	1366.33	5.8e-68	2301	L163075 Sus scrofa P-selectin m
gb_pat1:AF163766	+ 862.00	1365.33	6.8e-68	2650	AF163766 Sus scrofa P-selectin
gb_pat1:IT43650	+ 862.00	1342.57	1.3e-66	1833	I43650 Sequence 2 from patent
gb_pat1:HUMMLAM1A	+ 862.00	1335.99	2.9e-66	3834	M24726 Human endothelial leuk
gb_pat1:IT43649	+ 862.00	1335.94	3.0e-66	3854	I43649 Sequence 1 from patent
gb_pat1:HUMMLAM1A	+ 862.00	1335.94	3.0e-66	3854	M30640 Human endothelial leuk
gb_pat1:RABEPLAM	+ 861.00	1339.40	1.9e-66	2192	M91004 Rabbit endothelial leuk
gb_pat1:OCU3446	+ 860.50	1336.59	2.7e-66	2749	U34446 Oryctolagus cuniculus B
gb_pat1:DOGSELEC	+ 860.00	1332.59	4.5e-66	3939	L23087 Canis familiaris E-sele

gb_pat1:RATLEAM	+ 858.50	1331.67	5.1e-66	3351	L25527 Rattus norvegicus E-
gb_pat1:MUSELELEC	+ 857.00	1330.55	5.9e-66	2911	M87862 Mus musculus E-selec
gb_pat1:MUSELAM1B	+ 857.00	1328.27	7.9e-66	3759	M80778 Mouse ELAM-1 gene, c
gb_pat1:BOVSELEC	+ 849.50	1318.90	2.6e-65	2850	L12039 Bovine capillary E-s

seq\_name: gb\_pat1:AR060685

seq\_documentation\_block:

LOCUS AR060685 2259 bp DNA PAT 29-SEP-1999

DEFINITION Sequence 1 from patent US 5840844.

ACCESSION AR060685

VERSION AR060685.1 GI:5987135

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

SOURCE

BASE COUNT

ORIGIN

alignment\_scores:

Quality: 2116.00 Length: 372  
Ratio: 5.68 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

Alignment block:

US-09-119-209-2 x AR060685 ..  
Align seg 1/1 to: AR060685 from: 1 to: 2259

1 MettIlePheProTrpLysCysGlnSerTrpGlnArgAspLeuTrpAsn117	1 MettIlePheProTrpLysCysGlnSerTrpGlnArgAspLeuTrpAsn117
129 ATGATGTTTCATGAGAAATGTCAGACACCCAGAGGACTTATGAGACAT	129 ATGATGTTTCATGAGAAATGTCAGACACCCAGAGGACTTATGAGACAT
17 ePheLysLeuTrpGlyTrpTrpMetLeuCysCysAspPheLeuAla134	17 ePheLysLeuTrpGlyTrpTrpMetLeuCysCysAspPheLeuAla134
179 CTTCAGATGTTGGGGGAGACAAATGCTGTTGTGTATGTTCTCCAGAC	179 CTTCAGATGTTGGGGGAGACAAATGCTGTTGTGTATGTTCTCCAGAC
34 IsGlyThrTrpCysTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp	34 IsGlyThrTrpCysTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp
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REFERENCE 1 (bases 1 to 2259)
AUTHORS Bowen,B.R., Nguyen,T. and Lasky,L.A.
TITLE Characterization of a human homologue of the murine peripheral

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JOURNAL Lymph node homing receptor
MEDLINE J Cell Biol. 109 (1), 421-427 (1989)
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REFERENCE 1 (bases 1 to 2354)

AUTHORS Siegelman, M. H. and Weissman, I. L.  
TITLE Human homologue of mouse lymph node homing receptor: evolutionary conservation at tandem cell interaction domains  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86 (14), 5562-5566 (1989)  
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AUTHORS   Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
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TITLE      Cloning of the cDNA encoding L-selectin from nonhuman primates
JOURNAL   Unpublished
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AUTHORS   Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
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TITLE      Direct Submission
JOURNAL   Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia
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REFERENCE   1 (bases 1 to 2323)
AUTHORS    Camerini,D., James,S.P., Stamenkovic,I. and Seed,B.
TITLE      Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node homing
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AUTHORS Tedder, T.F.
TITLE Direct Submission
JOURNAL Submitted (09-NOV-1989) Tedder T.F
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2 (bases 1 to 2330)
AUTHORS Tedder, T.F., Isaacs, C.M., Ernst, T.J., Demetri, G.D., Adler, D.A. and
Distche, C.M.
TITLE Isolation and chromosomal localization of cDNAs encoding a novel
human lymphocyte cell surface molecule, LAM-1. Homology with the
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JOURNAL J. Exp. Med. 170 (1), 123-133 (1989)
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DEFINITION Sequence 1 from patent US 5808025.
ACCESSION AR040718
VERSION AR040718.1 GI:5960081
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2330)
AUTHORS Tedder, T.F. and Kansas, G.S.
TITLE Chimeric selectins as simultaneous blocking agents for component
JOURNAL Patent: US 5808025-A 1 15-SEP-1998;
FEATURES
Location/Qualifiers
BASE COUNT 661 a 522 c 487 g 660 t
ORIGIN

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Ratio: 5.611 Gaps: 0
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DEFINITION Sequence 1 from patent US 5834425.
ACCESSION AR054061
VERSION AR054061.1 GI:5978923
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2330)
AUTHORS Tedder, T.F. and Kansas, G.S.
TITLE Use of chimeric selectins as simultaneous blocking agents for
JOURNAL Patent: US 5834425-A 1 10-NOV-1998;
FEATURES
source location/qualifiers
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BASE COUNT 661 a 522 c 487 g 660 t
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Ratio: 5.611 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.118
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ACCESSION 170140
VERSION 170140.1 GI:3006275
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AUTHORS
TITLE
JOURNAL
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DEFINITION Pongo pygmaeus L-selectin mRNA, complete cds.
ACCESSION U73729
VERSION 073729.1 GI:1658017
KEYWORDS
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pongo.
REFERENCE
1 (bases 1 to 1119)
Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
Tsurushita,N.
Cloning of the cDNA encoding L-selectin from nonhuman primates
2 (bases 1 to 1119)
Budman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
Tsurushita,N.
Direct Submission
Submitted (08-OCT-1996) Protein Design Labs, Inc., 2375 Garcia
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 1119)
Hudman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
Tsurushita,N.
Cloning of the cDNA encoding L-selectin from nonhuman primates
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2 (bases 1 to 1119)
Hudman,J.I., Fu,H., Johnson,C.E., Thakur,A.B., Berg,E.L. and
Tsurushita,N.
Direct Submission
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Avenue, Mountain View, CA 94043, USA
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101 ValGlyThrAsnLysSerLeuThrGluGlu1a1aGluAsnTrpGlyAspG1 117
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117 yGluProAsnAsnLysLysAsnLysGluAspCysValGlu11eTrp11eL 134
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201 GlnAlaProGluLeuGly1YThrMetAspCysThrHisProPheGlyAsnPh 217
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601 GAGCCCCCGGAACCTGGTACATGACATGACATGACTCAACCCCTTGGAGACTT 650
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251 GlnProThrCysGlnVal11eGlnCysGluProLeuSerAlaProAspLe 267
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DEFINITION Papio hamadryas anubis L-selectin precursor mRNA, complete cds.
ACCESSION U52074
VERSION U52074.1 GI:1326148
KEYWORDS
SOURCE olive baboon.
ORGANISM Papio hamadryas anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Papio.
REFERENCE
AUTHORS Tsunushita,N., Fu,H. and Berg,E.L.
JOURNAL PCR cloning of the cDNA encoding baboon L-selectin
MEDLINE 97128794
REFERENCE
AUTHORS
JOURNAL
JOURNAL
JOURNAL
2 (bases 1 to 1510)
Tsunushita,N.
Direct Submission
Submitted (21-MAR-1996) Naoya Tsunushita, Protein Design Labs,
Inc., 2375 Garcia Avenue, Mountain View, CA 94043, USA
FEATURES
Source
location/Qualifiers
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BASE COUNT 467 a 328 c 349 g 366 t
ORIGIN
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Quality: 1992.00 Length: 372
Ratio: 5.443 Gaps: 0
Percent Similarity: 98.387 Percent Identity: 93.548
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us-09-119-209-2 x PHU52074
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|||||
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34 lsglythrlycstrprphrlyrhislyrSerGlyLysProMetAsnTrp 50
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179 ATGGAACCGACGCTGCGATTCATCATTAATTCGAAATCCATGAAGACTGG 228
51 GluArgAlaArgArgPheCysArgAspAsnTrpThrAspLeuValAla 67
|||||
229 CAAAGCCTAGAGATTCGCCGAGACAAATTTACACAGATTTAGTTCGCA 278
67 eGluAsnLysAlaGluIleGlyuTyrlleuGluLysThrleuProPheSera 84
|||||
279 ACAAACAAAGGAGAAATGAGTATCTGGAGAAAGACTCTGCTTCAGTC 328
84 rGserTyrTrpTrpIleGlyIleArgLysIleGlyLysIleTrpThr 100
|||||
329 CTCTTACTACTGATGATGCAATCCGAGATAGAGGCAATATGAGCACTGG 378
101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAspG 117
|||||
379 GTGGGAACCAACAATCTCTCACTCAAGACAGAGAACTGGGAGATGG 428
117 yGluPrAsnAsnLysLysAsnLysGluAspCysValGluIleTrpIle 134
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429 GGAGCCCAACACAAAGAAACAGAGAGACTGCGTGGAGATCTATATCA 478
134 yAsArgAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
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151 LysAlaAlaLeuCysTrpThrAlaSerCysGlnProTrpSerCysSerG 167
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167 yHisGlyLysCysValGluIleIleAsnAsnHisThrCysAsnCysAsp 184
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579 CCATGAGAAATGTGTAATAATCATCAATATTTACACCTGCAGACTGATG 628
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217 eSerPheSerSerGlnLysAlaPheSerCysSerGlyLysThrAsnLeu 234
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729 CAGCTTACGCTCACAGTGTGCTTCAACAGCTCTTGAGGAGAAACTTAA 778
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779 CTGGATTGAAGAAACACATTTGGACCATTTTGGAAACTGGTCATCTCA 828
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
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829 GAACCAACCTGTCAAGTGAATCAGTGTGAGCCTTATGACGACCAAGATT 878
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheHisSera 284
|||||
879 GGGATCATGAAGATGATGACACCCCTGGCCAGCTTCAGCTTTCCTTG 928
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267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSerA 284
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955 GGGGACCATTTGATGTAGTCATCCTCGGGCTGTCTTGGCTTTACTCTTA 1004
284 lAcYThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
: : : : : ||| : : : : : ||| : : : : : ||| : : : : : |||
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301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG 317
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1055 ACTGTTTCTGGATCATCTCGAATCTGGTCCAGTCTTACACCAAAATGTCA 1104
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1105 AAAAGTGGACAGAGCTTCTCTATGATCAAGAAGGTGACTATATACCCC 1154
334 eupheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
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1155 TCTTCATTCTCTGGCAGTCATGTAAGTCTCTCTGGGTTGGGCTTC 1204
351 IleIleTrpLeuAlaArgArgLeuLysGlyLysLysSerLysArgSe 367
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1205 ATCATTTGGCTGGCAAGCGACCTCAAAAAAGCAAGAAATCTCAGAAAAG 1254
367 rMetAsnAsp 370
| : : : |||
1255 CAAGGATGAC 1264
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OM of: US-09-119-209-2 to: N\_Geneseq\_36:\* out\_format : pfs

Date: Jan 13, 2001 3:10 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-MODEL=framed-p2n.model -DEV=xlp
-O/cg2_2/gcgdata/geneq/genseq/NA1993.rng -runat_08012001_083825_1992/app_query.fasta_1.434
-Dh=N_Geneseq_36 -OFMT=fasta -SUFFIX=ring -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FCGAPOP=6.000 -FCGAPEXT=7.000 -YGAPEXT=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MILEN=0 -MAXLEN=2000000000
-USBR=US09119209_@CGN1_1131 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPRX
-WAIT -THREADS=1
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Search information block:

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Query: US-09-119-209-2
Query Length: 372
Database: N_Geneseq_36:*
Database sequences: 480022
Database length: 18781343
Search time (sec): 89.970000
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seq\_documentation\_block:

ID Q43154 standard; cDNA; 2259 BP.

AC Q43154;

DT 08-OCT-1993 (first entry)

DE Human Lymphocyte Homing Receptor coding sequence.

KW HuLHR; Lymphocyte binding inhibition; Lymphoma metastasis;

KW Transplant rejection; ss.

XX Homo sapiens.

PH Key Location/Qualifiers

FT CDS 129..1247

FT /\*tag= a

FT /product= HuLHR

FT sig\_peptide 186..224

FT /\*tag= b

PN US5216131-A.

PD 01-JUN-1993.

PR 23-FEB-1989; 89US-0315015.

PR 23-FEB-1989; 89US-0315015.

PR 31-OCT-1991; 91US-0786149.

PA (GENE ) GENE TECH INC.

PI Lasky LA, Rosen SD, Singer MS, Stachel SE, Yednock TA;

DR WPI; 1993-188588/23.

PT P-PSDB; R37960.

PS Human and murine lymphocyte homing receptors to treat graft

PT rejection and inflammation - comprise carbohydrate binding,

PS epidermal growth factor and complement binding domains

XX Example 2; Fig 1; 32pp; English.

CC A human peripheral blood lymphocyte cDNA library in lambda gt10 was

CC screened with a 2.2kb EcorI Insert of the murine Mel1a antigen clone

CC (i.e. a murine LHR sequence). The largest EcorI Insert (2.2kb) was

CC isolated and sequenced. The ORF codes for 372 amino acids with a mol.

CC wt. of approximately 42,200. Comparison of the HuLHR cDNA with the

CC previously determined murine LHR sequence (Q43155) showed 83%

XX homology.

XX Sequence 2259 BP; 635 A; 515 C; 490 G; 619 T; 0 other;

SO Alignment\_scores:

Quality: 2116.00 Length: 372

Percent Similarity: 100.000 Gaps: 0

Percent Identity: 100.000

Alignment\_block:

US-09-119-209-2 x Q43154 ..

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17 ephelusleutripglytrpThrmleucscysaspheleuAlahsh 34  
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179 CTCAGATTGTGGGGTGGACATGCTGTGTTGTGATTCCTGGCACATC 228  
34 IsglythrycystripThryhisTyrSerglulysPrometasntrp 50  
229 ATGGAACCTACTGCTGACTTACATTATTTGAAAAACCATGAACTG 278  
51 GluAryAlaArgArphecysArgaspasntyrThraspleuValAla 67  
|||||  
279 CAAGGGGCTAGAAAGATTGTGCCGAGACAAATTACACAGATTAGTGCAT 328  
67 eglinasnlysalagluilegluTyrleuglulysThrleuProphesera 84  
|||||  
329 ACAAAACAAGCGCGAATGTGAGTATCTGAGAAAGACTGCGCTTACATC 378  
84 rgsertyrtyrtpilleglyllearglysileglyliletrpThrtp 100  
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379 GTTCTTACTACTGGATAGGAATCCGGAAGATAGAGGAATATGACCTGG 428  
101 ValGlyThrasnlyserleuthrgrgluAlaGluAsnTrpGlyAspG 117  
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429 GTGGGACCAACAATCTCTCACTGAGAGAGAGAACTGGGGAGATGG 478  
117 ygluProasnasnlyslsAsnlysgluAspCysValGluiletyrile 134  
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479 TGAAGCCCAACAAGACAGACAGAGAGAGCTGCGTGAGATCTATATCA 528  
134 yArGAsnlyspalaglylyTTPAsnAspAlaCysHisTysleu 150  
529 AGAGAAACAAGATGACGCAATGCAACGATGACGCTGCCACAAACCTA 578  
151 LysAlaAlaLeuCystyrThraserCysgluProtrpSerCysSerg 167  
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579 AAGGACAGCCCTGTGTACACAGCTTGTGCCAGCCCTGGTACAGAGTGG 628  
167 yHisglylucysValGluilelleasnAsnHisThrCysAsnlysp 184  
|||||  
629 CCATGAGAAATGTGTAGAAATCATCAATATGACACCTGCAACTGTGATG 678  
184 aIGlyTyrTyrGlyProglncysgluLeuValileglncysgluProleu 200  
679 TGGGGTACTATGGGCCCACTGTCAGCTTGATTCAGTGTGAGCCCTTGG 728  
201 GluAlaProgluLeuglyThrmleAspcysThrHisPropheglyAsnPh 217  
|||||  
729 GAGGCCCCAGAGCTGGGTACCATGAGCTGTACTACCCCTTTGGAACTT 778  
217 eSerPheSerSerglncysAlaPheSerCysSergluclyThrasnleut 234  
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779 CAGCTTCAGCTACAGTGTGCTTCACTGCTGTGAGAACCAACTTAA 828  
234 hrGlyilegluGluThrThrcysglyPropheglyAsnTrpSerSerPro 250  
829 CTGGGATTGAGAAACCACTGTCGACCATTTGGAACTGTCATCTCCA 878  
251 GluProThrcysgluValileglncysgluProleuSerAlaProaspLe 267  
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879 GAACCAACCTGTCAAGTATTCAGTGTGAGCTCTATCAGACCAAGATT 928  
267 uGlylleMetAsnlyserHisProleuAlaSerPheSerPheThrSera 284  
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929 GGGGATCATGAAGTACCATCCCTGGCAGCTTCAGCTTACCTGTG 978  
284 lacSthPheleleCysSerleuglyThrgluLeuileglyLysLyslys 300  
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979 CATGTACCTTATCTGCTCAGAGAACTGAGTTAATTTGGAGAAAGAAAA 1028  
301 ThrleCysgluSerSerglylleTrpSerAsnProserProleCysgl 317  
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1029 ACCATTGTGAAATCATCTGGAATCTGTCAAACTCTAGTCCAAATATGTCA 1078  
317 nLysleuAspLysSerPheSerMetileLysGluGlyAspTyrAsnProL 334  
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1079 AAAAATTGGACAAAGTTTCTCATATGATTAAGAGGGGTATTATTAACCCC 1128  
334 euPheileProValAlaValMetValIrnAlaPheSerSerglyLeuAlaPhe 350  
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seq\_documentation\_block:  
ID 044243 strand: DNA; 2259 BP.  
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AC 044243:  
XX  
DT 11-JAN-1994 (first entry)  
XX  
DE HULHR DNA.  
XX  
KW Human; murine; lymphocyte; cell surface glycoprotein; homing receptor;  
LHR; endothelium; lymphoid tissue; signal; domain; complement binding;  
carbohydrate binding; epidermal growth factor-like; egf; intracellular;  
KW transmembrane binding; cytoplasmic; ligand binding partner protein;  
TMD; LBPP; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 129..1247  
FT sig\_peptide 186..224 /\*tag= a  
FT mat\_peptide 243..1244 /\*tag= c  
FT FT  
PN US522538-A.  
XX  
PD 06-JUL-1993.  
XX  
PF 23-FEB-1989; 89US-0315015.  
XX  
PR 23-FEB-1989; 89US-0315015.  
PR 22-NOV-1989; 89US-0440625.  
PR 16-DEC-1991; 91US-0808122.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Capon DJ, Lasky LA;  
XX  
DR WPI: 1993-226664/28.  
DR P-PSDB: R38908.  
XX  
PT New lymphocyte homing receptor immunoglobulin fusion  
PT polypeptide(s) - used to inhibit binding of lymphocytes in  
PT therapeutic and diagnostic uses  
XX  
PS Disclosure: Fig 1; 44pp; English.  
XX  
CC The sequences given in 044243-44 encode human and murine lymphocyte  
cell surface glycoprotein (LHR) respectively. The proteins encoded  
by these sequences mediate the binding of lymphocytes to the  
endothelium of lymphoid tissue. LHR is a glycoprotein which contains  
a signal domain, a carbohydrate binding domain, an epidermal growth

CC factor-like (egf) domain, at least one complement binding domain  
 CC repeat, a transmembrane binding domain (TMD) and a charged intra-  
 CC cellular or cytoplasmic domain. The murine and human amino acid  
 CC sequences show a high degree of overall homology (83%), however  
 CC degrees of homology between the various domains is variable. These  
 CC proteins may be fused to a ligand binding partner protein (LBP) which  
 CC causes an increase in the half life of the LHR. The fusions may be  
 CC used therapeutically to compete with the normal binding of  
 CC lymphocytes to lymphoid tissue. They may be used in organ or graft  
 CC rejection and for the treatment of inflammation.

XX  
 SO Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

#### alignment\_scores:

Quality: 2116.00 Length: 372  
 Ratio: 5.688 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

#### alignment\_block:

US-09-119-209-2 x Q44243 ..

Align seg 1/1 to: Q44243 from: 1 to: 2259

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17 ePheLysLeuTrpGlyTrpThrMetLeuCysAspPheLeuAlaIleH 34
  |||
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  |||
34 IsGIYThrCysTrpTrpThrTrpIleTrpSerGlnLysProMetAsnTrp 50
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229 ATGGAACTACTGCTGAGACTTACCATTTATTCGAAAAACCCATGAACTG 278
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67 eGlnAsnLysAlaGluIleGlyTrpLeuGlnLysThrLeuProPheSerA 84
  |||
329 ACAAAACAGAGCGGAATGAGTATCTGGAGAAAGACTCTGCCCTTCAGAC 378
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101 ValGlyThrAsnLysSerLeuThrGlnLysAlaGluAsnTrpGlyAspG 117
  |||
429 GTGGGACCAACAAATCTCTCACTAGAAAGACAGAACTGGGAGATGG 478
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117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTrpIle 134
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479 TGAGGCCCAACAAGAAAGAACAGAGACACGCGTGAGATCTATATCA 528
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  |||
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167 yHisGlyLeuCysValGluIleIleAsnAsnHisThrCysAsnCysAsp 184
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  |||
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367 rMetAsnAspProTrp 372
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seq_documentation_block:
ID Q92802 standard; cDNA: 2259 BP.
XX
AC Q92802;
XX
DT 01-DEC-1995 (first entry)
XX
DE Human LHR cDNA.
XX
KW Lymphocyte homing receptor; lymphocyte cell surface glycoprotein;
KW LHR; ligand binding partner; immunoglobulin; constant region;
KW antibody engineering; immunomodulator; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 129..1247
FT FT /*tag= a
FT sig_peptide 186..224
FT FT /*tag= b
FT mat_peptide 243..1244
FT FT /*tag= c
XX
PN US5428130-A.
XX
PD 27-JUN-1995.
XX
PF 23-FEB-1989; 89US-0315015.

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XX 22-NOV-1989; 89US-0440625.  
 PR 23-FEB-1989; 89US-0315015.  
 PR 16-DEC-1991; 91US-0808122.  
 PR 08-DEC-1992; 92US-0986931.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Capon DJ, Lasky LA;  
 XX  
 DR WPI: 1995-240086/31.  
 DR P-PSDB: R76506.  
 XX  
 PT New hybrid ligand binding partner molecules - fused to immunoglobulin  
 PT constant region sequences to increase stability and in vivo plasma  
 XX half-life  
 PS Disclosure: Fig. 1a-1c; 40pp; English.  
 XX  
 CC A murine Mel 14 antigen cDNA clone was used to screen a lambda gt10  
 CC cDNA library derived from human peripheral blood lymphocyte mRNA  
 CC obtd. from primary cells. A cDNA clone encoding LHR was isolated.  
 XX  
 SQ Sequence 2255 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

## alignment\_scores:

Quality: 2116.00 Length: 372  
 Ratio: 5.688 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-119-209-2 x Q92802 ..

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 DT 31-JAN-1996 (first entry)  
 DT 705869;  
 XX  
 DE Human LHR cDNA.  
 DE  
 KW Lymphocyte cell surface glycoprotein; LHR: transmembrane receptor;  
 KW immunoglobulin; IgG: constant region; receptor-mediated disease;  
 KW vector; plasma-life; ss.  
 OS Homo sapiens.  
 OS  
 XX  
 PH key Location/Qualifiers



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FT /*tag= b
FT mat_peptide 243..1244
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XX US5455165-A.
XX
XX 03-OCT-1995.
XX
XX 23-FEB-1989; 89US-0315015.
XX
XX 22-NOV-1989; 89US-0440625.
XX 23-FEB-1989; 89US-0315015.
XX 16-DEC-1991; 91US-0808122.
XX 08-DEC-1992; 92US-0986931.
XX 21-JAN-1994; 94US-0185669.
XX
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA:
XX
XX WPI; 1995-350776/45.
XX
XX P-PSDB; R83050.
XX
XX Expression vector encoding fusion protein to increase plasma life -
XX PT comprises receptor ligand binding site and Ig constant region, for
XX PT treatment of receptor mediated disease
XX
XX PS Disclosure; Fig 1; 42pp; English.
XX
XX CC A mouse LHR (lymphocyte cell surface glycoprotein) cDNA clone was used
XX CC to screen an oligo-dT primed lambda gt10 cDNA library derived from
XX CC human peripheral blood lymphocyte mRNA obtd. from primary cells. A
XX CC 2.2 kb clone (sequence given in T05869) showing 83% DNA sequence
XX CC homology to the murine LHR gene (T05870) was isolated. The LHR genes
XX CC are used to construct LHR-IgG hybrids used to target therapeutic
XX CC moieties to lymphoid tissue.
XX
XX SQ Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

Alignment_scores:
Quality: 2116.00 Length: 372
Ratio: 5.688 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
729 GAGGCCCCAGAGCTGGGTACATGAGACTGACTACACCCCTTGGAAACTT 778
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1029 ACCATTGTGATTCATCTGGATCTGGTCAAAATCCCTAGTCCATATATGCTA 1078
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334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
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seq\_documentation\_block:

ID T30003 standard; DNA: 2259 BP.

AC T30003;

XX 31-OCT-1996 (first entry)

XX Human lymphocyte cell surface glycoprotein (HULHR) coding sequence.

XX Immunoglobulin; transmembrane receptor; adhesion; targeting;  
 KW diagnosis; therapy; drug delivery; antiviral; neuromodulator;  
 KW immunomodulator; cell adhesion; graft rejection; inflammation;  
 KW metastasis; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 129..1247

FT sig\_peptide 129..242 Lymphocyte cell surface glycoprotein.

FT mat\_peptide 243..1244

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XX US5514582-A.

XX 07-MAY-1996.

XX 23-FEB-1989; 89US-0315015.

XX 22-NOV-1989; 89US-0440625.

XX 23-FEB-1989; 89US-0315015.

XX 16-DEC-1991; 91US-0808122.

XX 08-DEC-1992; 92US-0986931.

XX 21-JAN-1994; 94US-0185670.

XX (GETH ) GENENTECH INC.

XX Capon DJ, Lasky LA;

XX WPI: 1996-238773/24.

XX P-PSDB: R98106.

XX Nucleic acid encoding hybrid immunoglobulin comprising the ligand

XX binding site of a receptor fused to Ig constant region - useful for

XX diagnosis and treatment e.g. of inflammation

XX Example 2; Figure 1; 41pp; English.

XX A hybrid immunoglobulin chain comprising the ligand binding site of  
 CC a single transmembrane receptor without an active transmembrane  
 CC region; fused at its C-terminus with the N-terminus of an  
 CC immunoglobulin constant region. The receptor is not a member of the  
 CC immunoglobulin super family, nor a multiple subunit polypeptide  
 CC encoded by discrete genes. The hybrid immunoglobulin chain combines  
 CC effector functions of immunoglobulin and can bind to and/or activate  
 CC more than one ligand. It can be used diagnostically for the in  
 CC vitro assay of LBP and their targets; or therapeutically to deliver  
 CC LBP such as toxins, enzymes, growth factors to particular cells.  
 CC Typical applications are as antiviral, neuromodulating and  
 CC immunomodulating agents, or as modulators of cell adhesion (e.g. in  
 CC treating graft rejection; inflammation; metastasis of lymphoma etc.)  
 CC The immunoglobulin component increases plasma half life and  
 CC facilitates purification while deletion of the transmembrane region  
 CC potentially immunogenic epitopes.

XX Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other;

alignment\_scores:

Quality: 2116.00

Ratio: 5.688

Percent Similarity: 100.000

Percent Identity: 100.000

alignment\_block:

US-09-119-209-2 x T30003 ..

Align seg 1/1 to: T30003 from: 1 to: 2259

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579 AAGCACCCCTCTGTATACACAGCTTCTTCCACGCCCTGGTCATGACGTG 628
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629 CCATGGAGAAATGTGMAAATTCATATATTCACACCTCAACTGATGGATG 678
184 aGlyTrrTrrGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
679 TGGGATCTATGGGCCCACTGACCTTGTATTTAGTGTAGCTTTTG 728
201 GluAlaProGluLeuGlyThrMetAspCysTrrHisProPheGlyAsnPh 217
729 GAGGCCCAAGAGCTGGGTACCATGACTGTACACCCCTTTGGAACCT 778
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuT 234
779 CACTTTCAGCTCAGCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCT 828
234 hrgLylIleGluGluTrrThrCysGlyProPheGlyAsnTrrSerSerPro 250
829 CTGGATTGAAAGAACCACTGTGGACCATTTTGGAACAGGTCATCTCCA 878
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267

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879  GAACCAACCTGTCAAGTATTCAGTGTGAGCCTCATACGACACGAGATT 928
267  uGlyllemetascysSerHisProleuAlaserPheSerPheThrSera 284
929  GGGGATCATGAACTTACCCATCCCTGCGCAGCTTACCTTACCTCTCG 978
284  lAcysThPheIlleCysSerGluGlyThrGluLeuIlleGlyLysLys 300
979  CATGACCTTCATCTGCTCAGAAAGAACTGACTGAATTGCGAAGAA 1028
301  ThrIlleCysGluSerSerGlyThrPheSerAsnProSerProIlleCys 317
1029  ACCATTTCGATTCATCTGGAATCTGCTCAATTCCTAGCCAAATGTGTA 1078
317  nLysLeuAspLysSerPheSerMetIlleLysGluLysAspTrpAsnPro 334
1079  AAAATTGGACAAAGTTTCTCTCAATGATTATAGGAGGCTGATTAAACCC 1128
334  euPheIlleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
1129  TCTTCATTCACACTGGCAGTCATGTTACTGCAWCTCTCGCTTGGCATTT 1178
351  lIlelletTrpLeuAlaArgArgLeuLysLysGlyLysLysSerLysArgSe 367
1179  ATCATTTTGGCTGGCAAGGAGATTAAAAAAGCAAGAAATCCAGAGAGAG 1228
367  rMetAsnAspProTyr 372
1229  TATGATGACCCCATAT 1244

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seq\_documentation\_block:

ID V19012 standard; DNA; 2259 BP.

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XX AC V19012:
XX DT 17-AUG-1998 (first entry)
XX DE Homo sapiens lymphocyte homing receptor (LHR) gene.
XX KW lymphocyte homing receptor; LHR; HuLHR; organ; graft; rejection;
XX KW treatment; inflammatory disorders; rheumatoid arthritis;
XX KW autoimmune diseases; lymphoma metastasis; control; lymphocyte;
XX KW accumulation; ds.
XX OS Homo sapiens.
XX FI Key Location/Qualifiers
XX FT CDS 129..1247
XX FT /tag= a
XX FT /product= lymphocyte homing receptor
XX PN US5714147-A.
XX PD 03-FEB-1998.
XX PF 23-FEB-1989; 89US-0315015.
XX PR 22-NOV-1989; 89US-0440625.
XX PR 23-FEB-1989; 89US-0315015.
XX PR 19-DEC-1991; 91US-0808122.
XX PR 08-DEC-1992; 92US-0986931.
XX PR 21-JAN-1994; 94US-0185670.
XX PR 26-MAY-1995; 95US-0451848.
XX PA (GETH ) GENENTECH INC.
XX PI Capon DJ, Lasky LA;
XX DR WPI; 1998-129805/12.
XX P-PSDB; W37781.
XX

```

PT Prevention of lymphocyte attachment to endothelial cells - using  
PT chimeric molecule comprising lymphocyte homing receptor and  
PT immunoglobulin constant region  
XX  
PS Disclosure: Fig 1; 43pp; English.

XX  
CC The sequence is that encoding a human lymphocyte homing receptor  
CC (LHR) which may be used in the construction of a chimeric molecule  
CC comprising an LHR fused at its C terminus to the N terminus of an  
CC immunoglobulin constant region. This can be used for the prevention  
CC of lymphocyte attachment to endothelial cells. Such a method may  
CC be used for preventing organ or graft rejection, for treating  
CC inflammatory disorders, e.g. rheumatoid arthritis or other  
CC autoimmune diseases, for controlling lymphoma metastasis and  
CC for treating conditions in which there is an accumulation of  
CC lymphocytes.

XX Sequence 2259 BP; 635 A; 516 C; 489 G; 619 T; 0 other:

alignment\_scores:

Quality:	Ratio:	Length:	Gaps:
2116.00	5.688	372	0
Percent Similarity: 100.000	Percent Identity: 100.000		

alignment\_block:

US-09-119-209-2 x V19012

Align seg 1/1 to: V19012 from: 1 to: 2259

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179 CTTCAAGTTGTGGGGGTGGACAATGCTCTGTGTGATTTCCTGGCACAATC 228
34 lSGlyThrTrpCysTrpThrTrpHisLysSerGluLysProMetAsnTrp 50
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51 GlnAArgAlaArgArgPheCysArgAspAsnTrpTrpAspLeuValAlaIl 67
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329 ACMAAACAAGCGCGAAATGAGTATCTGGAGAAAGACTTGGCCTTCAGATC 378
84 rGSetrTyrTrpTrpIlleGlyTrpLeuArgLysIlleGlyGlyLeuTrpThrTrp 100
379 GTTCTTACTACTGATAGGAATCCGGAATAGGAGATATGAGCACTGCG 428
101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAspGIl 117
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117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIlleTyrIle 134
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579 AAGGACGCCCTCTGTACACAGCTTCTTGCCAGCCCTGGTACATGACATGG 628
167 yHisGlyGluCysValGluIlleLeuAsnAsnHisThrCysAsnAspV 184
629 CCATGGAGATGTGTGAATCATCATCAATATCAACCTGCAACTGTGATG 678

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779 CAGCTTACGCTCACAGTGTGCTTACAGCTGCTGTAAGAGAACAACTTAA 828
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879 GAACCAACCTGTCAAGTATTCAAGTGTGAGCTCTATCACACCAAGATT 928
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979 CATGTACTTCACTGTCTGAGAAAGAACTGATTAATTGGGAAGAGAA 1028
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1179 ATCATTTTGGCTGGCAAGAGATTAATAAAAGCAAGAAATCCAAAGAGA 1228
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seq_documentation_block:
ID V08321 standard; DNA; 2259 BP.
XX
AC V08321;
XX
DT 02-FEB-1999 (first entry)
XX
DE Human lymphocyte homing receptor coding sequence.
XX
KW Lymphocyte homing receptor; LHR; lymphocyte cell-surface glycoprotein;
KW lymphocyte binding; endothelium; graft rejection; inflammation; therapy;
KW arthritis; autoimmune disease; lymphoma metastasis;
KW lymphocyte accumulation; human; ss.
XX
OS Homo sapiens.
XX
PN US5840844-A.
XX
PD 24-NOV-1998.
XX
PF 10-AUG-1995; 95US-0513278.
XX

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PR 23-FEB-1989; 89US-0315015.
PR 31-OCT-1991; 91US-0786149.
PR 06-MAY-1993; 93US-0059029.
PR 10-AUG-1995; 95US-0513278.
XX
XX (GETH ) GENENTECH INC.
XX (REGC ) UNIV CALIFORNIA.
XX
PI Lasky LA, Rosen SD, Singer MS, Stachel SE;
XX WPI; 1999-034122/03.
XX DR P-PSDB; W73264.
XX
XX Lymphocyte homing receptor polypeptides - useful for inhibiting
XX Lymphocyte binding to lymphoid endothelium
XX
XX Disclosure; Fig 1; 33pp; English.
XX
XX This sequence encodes the human lymphocyte homing receptor (LHR) of the
XX invention. LHR is a lymphocyte cell-surface glycoprotein that mediates
XX the binding of lymphocytes to the endothelium of lymphoid tissue. Soluble
XX LHR polypeptides, lacking signal peptide (amino acids 1-38),
XX transmembrane domain (amino acids 333-355) and cytoplasmic domain (amino
XX acids 356-372), can be used therapeutically to compete with the normal
XX binding of lymphocytes to lymphoid tissue and are especially useful for
XX organ or graft rejection treatment protocols, for treating inflammations
XX such as arthritis and other autoimmune diseases, for control of lymphoma
XX metastasis and for treating conditions involving lymphocyte accumulation.
XX LHR polypeptides can also be used in assays for LHR, anti-LHR antibodies
XX or competitive inhibitors of LHR activity, and for purifying anti-LHR
XX antibodies, and as immunogens for raising anti-LHR antibodies.
XX
XX SO Sequence 2259 BP; 635 A; 517 C; 488 G; 619 T; 0 other.
XX
XX alignment_scores:
XX      quality: 2116.00      length: 372
XX      ratio: 5.688      gaps: 0
XX      Percent Similarity: 100.000      Percent Identity: 100.000
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XX alignment_block:
XX US-09-119-209-2 x V08321 ..
XX
XX Align seq 1/1 to: V08321 from: 1 to: 2259
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XX 1 MetIlePheProTrpLysCysGlnSerThrGlnArgAspLeuTrpAsnI 17
XX |||
XX 129 ATGATATTTTCATGCAAAATGTCAGAGCACCCAGAGGACTTATGGAAACAT 178
XX |||
XX 17 ePheLysLeuTrpGlyTyrThrMetLeuCysCysAspPheLeuAlaHis 34
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XX 179 CTTCAGATTGTGGGGGTGAGCAATGCTGTGTGATTTTCGCGCACATC 228
XX |||
XX 34 IsGlyThrTyrCysTrpThrTyrHisTyrSerGluLysProMetAsnTrp 50
XX |||
XX 229 ATGGAACTTACTGCTGGACTTACCATTAATTCGAAAAACCATGAATCG 278
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XX |||
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XX |||
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XX |||
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XX |||
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XX |||
XX 101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAspG 117
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XX |||

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134 ysArGAsnLysAspAlaGlyLysTrpAsnAspAlaCysHisLysLeu 150
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529 AGAGAAACAAAGATCAGCAAAATGMAAGATGAGCCGCAACAAACTA 578
151 LysAlaAlaLeuCysTyrThrAlaSerCysGlnProTrpSerCysSerG 167
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579 AAGGACGCCCTCTGTTACACAGCTTCTTCCAGCCCTGCTACGACGTGG 628
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|||||
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1029 ACCATTTGTGAATCATCTGCAATCTGTCAAAVCTTACCTAGTCCAAAT 1078
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrAsnProL 334
1079 AAAATTTGCACAAAACTTCTCTCAATGATTAAAGAGAGGTATTATAACCC 1128
334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
1129 TCTTCATTCAGTGTGACATGATGTTACTGTCTCTGGGTGGCATTT 1178
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seq_documentation_block:
ID Q24987 standard: DNA; 2262 BP.
XX
AC Q24987;
XX
DT 22-NOV-1992 (first entry)
XX
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DE Sequence encoding human lymphocyte cell surface glycoprotein
DE (HuLHR).
DE
XX Lymphocyte cell surface glycoprotein; ligand binding protein; ss.
XX
XX Homo sapiens.
XX
OS
XX Key CDS
XX CDS
XX sig_peptide
XX mat_peptide
XX
XX US5116964-A.
XX
XX 26-MAY-1992.
XX
XX 22-NOV-1989; 89US-0440625.
XX
XX 23-FEB-1989; 89US-0315015.
XX 22-NOV-1989; 89US-0440625.
XX (GETH ) GENENTECH INC.
XX
XX Capon DJ, Lasky LA;
XX
XX WPI: 1992-199589/24.
XX P-PSDB: R24026.
XX
XX Nucleic acid encoding polypeptide fusions - comprising ligand
XX binding partner protein and immunoglobulin chain, for use in
XX diagnosis and therapy
XX
XX Disclosure: Fig 1-1 - 1-3; 43pp; English.
XX
XX LHR mediates the binding of lymphocytes to the endothelium of
XX lymphoid tissue. Full length cDNA clones and DNA encoding the human
XX CC and the murine LHR (HuLHR and MLHR, respectively) have been
XX CC identified and isolated (see Q24987 and Q24988). LHR is a
XX CC glycoprotein which contains the following protein domains: a signal
XX CC sequence, a carbohydrate binding domain, and epidermal growth
XX CC factor-like (egf) domain, at least one and preferably two complement
XX CC binding domain repeat, a transmembrane binding domain (TMD), and a
XX CC charged intracellular or cytoplasmic domain. LHR is used as the
XX CC ligand-binding partner in fusion polypeptides with an immunoglobulin,
XX CC for use in diagnosis and therapy.
XX
XX SO Sequence 2262 BP; 635 A; 518 C; 488 G; 621 T; 0 other.
XX
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XX Quality: 2109.00 Length: 372
XX Ratio: 5.685 Gaps: 0
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XX alignment_block:
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151  LysAlaAlaLeuCysTyrThrAlaSerCysGlnProTrpSerCysSerGly 167
579  AAGGAGCCCTCTGTACACAGCTTCTTCCAGCCCTGGTCAATGCAAGTGG 628
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979  CATGTACCTTCATCTGCTCAGAACAGAACTGATTAATTGGGAAGAAACAA 1028
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XX   Q23623;
AC   Q23623;
DE   01-SEP-1992 (first entry)
XX   Human lymphocyte homing receptor gene.
XX   HUHR; LHR; binding; endothelium; immunogens; graft; organ; ss;
XX   rejection; inflammation; rheumatoid arthritis; lymphoma metastasis.
XX   Homo sapiens.
XX   Key Location/Qualifiers
XX   CDS 129..1248
XX   /tag= a
XX   US5098833-A.
XX   24-MAR-1992.
XX   23-FEB-1989; 89US-0315015.
XX   23-FEB-1989; 89US-0315015.
XX   (REGC ) UNIV OF CALIFORNIA.
XX   Lasky LA, Rosen SD, Stachel SE, Singer MS, Yednock TA;
XX   WPI: 1992-123385/15.
XX   P-PSDB; R22802.
XX   New DNA encoding at least one domain of lymphocyte homing
XX   receptor - useful for treating graft rejection, inflammation,
XX   etc.
XX   Claim 3; Fig 1; 32pp; English.
XX   The DNA sequence was obt'd. by screening an oligo dT primed lambda
XX   gt10 cDNA library derived from human peripheral blood lymphocyte
XX   mRNA obt'd. from primary cells, with a 2.2 kb EcoRI insert of the
XX   murine Mel 14 antigen cDNA clone. 12 positive plaques were isolated
XX   and those with the largest EcoRI insert were sequenced. The 2.2 kb
XX   clone encodes an open reading frame of 372 amino acids. The human
XX   LHR is 83 percent homologous with the murine LHR sequence and
XX   contains regions encoding a carbohydrate binding domain, an EGF-like
XX   domain, a complement binding domain and a transmembrane domain.
XX   Cells transformed by the huHR DNA are used to produce LHR (which
XX   mediates binding of lymphocytes to the endothelium of lymphoid
XX   tissue). LHR or its variants are useful as reagents for assaying
XX   LHR or anti-LHR antibodies, to purify the antibodies, as immunogens,
XX   and therapeutically to compete with normal binding of lymphocytes
XX   (to prevent graft/organ rejection; to treat inflammation (such as
XX   rheumatoid arthritis or other autoimmune diseases); for control of
XX   lymphocyte metastasis, and to treat conditions associated with
XX   accumulation of lymphocytes). Derivs. and variants of LHR may be
XX   produced having modified properties, e.g. increased activity, longer
XX   plasma half-life, reduced side effects and better ag. solubility.
XX   See also Q23624 and Q23464.
XX   Sequence 2260 BP; 636 A; 518 C; 487 G; 619 T; 0 other;

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## alignment\_scores:

Quality: 2108.00      Length: 372  
 Ratio: 5.667      Gaps: 0  
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## alignment\_block:

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Align seg 1/1 to: Q23623 from: 1 to: 2260

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179 CTTCACATGTGTGGGCTGGACAAATGCTGTGTCTGATTTCTCGCACATC 228
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34 1AsGlyThrTyrcysTrpThrTyrcHisTyrcSerGluLysPromeLanTrp 50
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51 GlnArgAlaArgArgPheCysArgAspAsnTyrrThrAspLeuValAlaI 67
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67 eGlnAsnLysAlaGluIleGluTrleuGluLysThrLeuProPheSerA 84
  |||
329 ACAAAACAAGCGCGAATATGAGTATCTGAGAGAGACTGCTGCCCTTCAGTC 378
  |||
84 rGserTyrrTyrrPrlleGlyIleArgLysIleGlyLysIleTrpThrTrp 100
  |||
379 GTTCTTACTACTGATNGAATCCGGAATGAGAGATNTGACGCTGG 428
  |||
101 ValGlyThrAsnLysSerLeuThrGluAlaGluAsnTrpGlyAspGly 117
  |||
429 GTGGCAACCAACAATCTCTCACTGAAGCAAGCAGACACTGGGAGATCG 478
  |||
117 yGluProAsnAsnLysLysAsnLysGluAsnLysValGluIleTyrlle 134
  |||
479 TCAGCCCAACAACAAAGAGAACAGACGAGCGCTGAGATCTTAATATCA 528
  |||
134 yAsrGsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
  |||
529 AGAGAAACAAGAATGCGCAAAATGGAACGATGACGCTGCCCAAACTA 578
  |||
151 LysAlaAlaLeuCysTyrrThrAlaSerCysGlnProTrpSerCysSerG 167
  |||
579 AAGCGAGCCCTCTGTACACAGCTTCTGCCAGCCCTGGTCATGACGTGG 628
  |||
167 yHisGlyLysValGluIleLeuAsnAsnHisThrCysAsnCysAspY 184
  |||
629 CCATGGAGAAATGTGTAAGAAATCATCAATATCACACCTCACTGTGATG 678
  |||
184 aLcIlyTyrrGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
  |||
679 TGGGGTACTATGGGCCCCAGTGTCACTGTGATTCAGTGTGACCTTTGG 728
  |||
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
  |||
729 GAGGCCCCAGACCTGGGTACATGACCTGTACTACACCCCTTTGAAACT 778
  |||
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuT 234
  |||
779 CAGCTTCACACTCACAGTGTGCTTCAGCTGTCTGTAAGCAACAACATTA 828
  |||
234 hrcGlyIleGluGluTrpThrCysGlyProPheGlyAsnTrpSerSerPro 250
  |||
829 CTGGGATTTAAGAAACCACTGTGAGCACTTTGGAAACTGGTCATCTCCA 878
  |||
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
  |||
  
```

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879 GAACCAACCTGTCAAGTATTCAGTGTGAGCCTCTATCAGCACACAGATTTT 928
267 uGlyIleMetLysCysSerHisProLeuAlaSerPheSerPheThrSerV 284
  |||
929 GGGGATCATGAACTGTAGCCATCCCTGGCAGCTTCAAGCTTACCTCTGG 978
  |||
284 1AcYrrPheIleCysSerGluGlyThrGluLeuIleGlyLysLysLys 300
  |||
979 CATGTACCTTCATCTGCTCAGAAAGAACTGAGTTATTTGGGAACAAGAAA 1028
  |||
301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG 317
  |||
1029 ACCATTTGTGAATCATCTGGAATCTGTGCAAAATCTCAGTCCAAATATG 1078
  |||
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTrpAsnProL 334
  |||
1079 AAAATTTGACAAANAGTTTCTCAATGATTTAAGAGGAGTATTAATACCCC 1128
  |||
334 eUpheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
  |||
1129 TCTTCATTCACATGCGCAGTCATGTTACTGCAATTTCTGGGTTGGCATTT 1178
  |||
351 IleIleTrpLeuAlaArgArgLeuLysGlyLysLysSerLysArgse 367
  |||
1179 ATCATTTTGGCTGGCAAGAGATTAATAAAAAAGCAAGAAATCCAAAGAGA 1228
  |||
367 rMetAsnAspProTyrr 372
  |||
1229 TATGAATGACCCATAT 1244
  |||
seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1991.DAT:012118
seq_documentation_block:
ID Q12118 standard; DNA: 2259 BP.
XX
XX Q12118:
XX
AC Q12118:
XX
AC Q12118:
XX
DT 09-SEP-1991 (first entry)
XX
DE Sequence encoding human lymphocyte cell surface glycoprotein (LHR).
XX
KW Ligand binding partner; lbp: stable plasma protein; spp: antiviral;
KW immunomodulatory; neuromodulatory; receptor mediated abnormality; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 129..1247
FT /*tag= a
FT sig_peptide 186..224
FT /*tag= b
FT mat_peptide 243..1244
FT /*tag= c
XX
XX MO9108298-A.
XX
XX PD 13-JUN-1991.
XX
XX PF 21-NOV-1990; 90WO-US06849.
XX
XX PR 22-NOV-1989; 89US-0444625.
XX
XX PA (GETH ) GENENTECH INC.
XX
XX PI Capon DJ, Tasky LA:
XX
XX WP1: 1991-193202/26.
XX
XX DR P-PSDB; R12469.
XX
XX PT New hybrid immunoglobulin(s) - for use as diagnostic reagents for
XX ligand binding molecules and to treat organ and graft rejection
XX
XX
  
```

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PS      Disclosure; Fig 1; 67pp; English.
XX      CC
XX      CC The gene product may be used as a ligand binding partner in combina-
XX      CC tion with a stable plasma protein eg IgG1-IgG4, IgA, IgE, IgD or IgM.
XX      CC The fusion product is joined by N- or C-terminal groups, preferably
XX      CC the N-terminal of the Fc region of the ssp is linked to the C-terminal
XX      CC of lbp. They may be used to provide antiviral, immunomodulatory
XX      CC and neuromodulatory treatment as well as in treatment of receptor
XX      CC mediated abnormalities.
SQ      Sequence 2259 BP; 634 A; 516 C; 487 G; 618 T; 4 other:

alignment_scores:
      Quality: 2095.00      Length: 372
      Ratio: 5.662      Gaps: 0
      Percent Similarity: 99.462      Percent Identity: 99.462

alignment_block:
US-09-119-209-2 x Q12118 ..

Align seg 1/1 to: Q12118 from: 1 to: 2259

1 MetIlePheProTrpLysCysGlnSerThrGlnArgAspLeuTrpAsnIle 17
129 ATGATATTTCATGSAATGTCACAGCCACCGAGGAGCTTATGGAACAT 178
17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHisH 34
179 CTTCAGATTGTGGGGGTGGACAAATGCTGTGTGATTTCTCTGGCAATC 228
34 ISGlyThrTrpCysTrpThrTrpHisTrpSerGluLysProMetAsnTrp 50
229 ATGGAACCTACTGCTGAGACTTACCATTTATCTGAAAAACCATGAATCG 278
51 GlnArgAlaArgArgPheCysArgAspAsnTrpThrAspLeuValAlaI 67
279 CAAGGGCTAGAAAGATTCTCCCGACAAATTACACAGATTATTGCGCAT 328
67 eGlnAsnLysAlaGluIleGluTrpLeuGluLysThrLeuProPheSer 84
329 ACAAAACAAGCGGAAATGAGTATCTGGAGAAAGACTCTGCCCTTCAGTC 378
84 rGSerTrpTrpTrpIleGlyIleArgLysIleGlyLysIleTrpTrp 100
379 GTTCTTACTACTGATAGGAAATCCGGAAGATGAGAAATATGAGACGTGG 428
101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAsp 117
429 GTGGGAAACCAAAATCTCTCACTGAAGAGCAAGAACTGCGGAGATGG 478
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTrpLe 134
479 TGAGCCCAACACAAAGACAGACAGAGAGCNGCGTGAGATCTATATCA 528
134 yArgGlnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
529 AGGAAACAACAAATGTCAGCAATGGAACGATGAGCCTGCACAAACTA 578
151 LysAlaAlaLeuCysTrpThrAlaSerCysGlnProTrpSerCysSer 167
579 AAGGACAGCCCTCTGTTACACAGACTTCTTGCCAGCCCTGTCATCAGTGG 628
167 yHisGlyLysCysValGluIleLeuAsnAsnHisThrCysAsnCysAsp 184
629 CCATGAGAAATCTGTAGAAATCATCAATATATACACCTGCACACGTGATG 678
184 aGlyTrpTrpGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
679 TGGGTTACTATGGGCCCCAGTGTGAGCTGTGATTCAGTGTGAGCCCTTGG 728
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProGlyAsnPh 217
|||||
729 GAGGCCCCAGAGCTGGGTACCATGAGACTGACTGACTCACCCTTTGAAACTT 778
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuT 234
779 CAGCTTACGCTCAGACTGATGCTTCTTCACTGCTGCTGAAAGAACAACTTAA 828
234 hrcGlyIleGluGluTrpThrCysGlyProPheGlyAsnTrpSerSerPro 250
829 CTGGGATTGAAAGAACCACTGTGGACATTGTGAAACCTGGTCACTCTCA 878
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
879 GAAACAACCTGTCAAGTCAATGATGAGCCCTCATCAGCACCAAGATTT 928
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSera 284
929 GGGATCATGAACTGAGGCATCCCTGGCCAGCTTCAAGCTTACCTGTG 978
284 lAcSerThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
979 CATGTAACCTTCATCTGCTCAGAGAGAACTGAGTTAATTGGGAAGAAAGA 1028
301 ThrIleCysGluSerSerGlyIleThrSerAsnProSerProIleCysG 317
1029 ACCATTGTGAAATCATCTGGAATCTGGTCAATCTAGTCCAAATATGTCA 1078
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTrpAsnPro 334
1079 AAAATTGGACAAAGTTTCTCAATGATTAAAGAGGGTGATTAATACCCC 1128
334 ePheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
1129 TCTTCATTCCAGTGGCAGCTCATGTGTTACTCATCTCTGTGGTTGGCATTT 1178
351 IleIleTrpLeuAlaArgArgLeuLysGlyLysLysSerLysArgSe 367
1179 ATCATTTGGCTGGCAAGACATTAAAAAAGGCAAGAAATCCAGAGAGAG 1228
367 rMetAsnAspProTrp 372
1229 TATGAAATGACCCATAT 1244

seq_name: /cgn2_2/gcdata/geneseq/geneseqn/NA1992.DAT:Q21184
seq_documentation_block:
ID Q21184 standard; DNA: 2350 BP.
XX
AC Q21184:
XX
XX
DT 21-MAY-1992 (first entry)
XX
XX Encodes T lymphocyte-specific Leu8 Antigen major form.
XX
DE Rapid immunoselection cloning technique: cell surface antigen;
XX
KW homing receptor; antigen-presenting cells; ss.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT CDS 50..1207
FT FT /**tag= a
XX
XX
XX M09201049-A.
XX
XX 23-JAN-1992.
XX
XX
XX 15-JUL-1990; 90MO-US04986.
XX
XX 13-JUL-1990; 900S-0553759;
XX
XX (GEHO-) GEN HOSPITAL CORP.
XX
XX Seed B, Arufo A, Amiot M,
XX
PI

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XX  WPI: 1992-056864/07.
DR  P-PSDB: R20815.
XX
PT  New CD53 cell surface antigen and DNA encoding it - for
XX  immuno-therapy and diagnosis of haematopoietic neoplasms, etc.
PS  Example 14: Page 106; 160pp; English.
XX
CC  Two cDNA clones encoding Leu8 determinants were isolated from a
CC  human T cell library using the rapid immunoselection cloning method
CC  (see e.g. Q21164 for description of method). The shorter insert
CC  (see Q22500) lacks 436 internal residues (i.e. nucleotides 1079 to
CC  1514 of the longer insert). RNA blot hybridisation
CC  revealed a major transcript of 2.4kb in peripheral blood
CC  mononuclear cells, tonsillar B cells and the Jurkat and HSB-2
CC  leukaemic T cell lines. A minor transcript of 2.0kb was present in
CC  peripheral blood mononuclear cells and the Jurkat and HSB-2
CC  leukaemic T cell lines. The protein encoded by the larger insert
CC  is closely related to the murine Mel-14 homing receptor.
XX
S0  Sequence 2350 BP: 679 A; 519 C; 490 G; 662 T; 0 other:

alignment_scores:
      Quality: 2082.00      Length: 372
      Ratio: 5.627          Gaps: 0
      Percent Similarity: 99.462      Percent Identity: 98.656

alignment_block:
US-09-119-209-2 x Q21184 ..
Align seg 1/1 to: Q21184 from: 1 to: 2350

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167 yhisglglucysvalgluileleasnansnhsrhcysasnrcysaspy 184
|||||
589 ccattgagaaatgctgtagaaatcatcaataatattacactgcactgcatg 638
|||||
184 aiegltyrtyrglyproglncysgluleuvalleleincysgluproleu 200
|||||
639 tggggtactatggggcccgactgctgctgctgctgctgctgctgctg 688
|||||
201 glualaprogluenuglythrmetascysrthnhsrphoeleynsnh 217
|||||
689 gagggcccgagctgggtacatgactgactgactgactgactgactg 738
|||||
217 eserpheserSerGlncysalapheserCysSerGllyThrAsnLeu 234
|||||
739 cacttgcactgcactgactgcttgcactgcttgcactgactgactg 788
|||||
234 hcglylleleugluthrthrcysglyprophelyasntrpserSerPro 250
|||||
789 ctgggattgagaaaccactggtgacatttggaactggtcattccca 838
|||||
251 gluprothrCysGlnValleleincysgluproleuSerAlaProAsp 267
|||||
839 gaaccacacctgctcagtgattcagctgagccctatcagcacacgatt 888
|||||
267 uglyllemetasnCysSerHisProleuAlaSerPheserPhetSerA 284
|||||
889 ggggagatcatgaaactgtagccatccctggccagacttgcactttacc 938
|||||
284 lacysThrPhelieCysSerGllyThrGluLeuilelelylsyls 300
|||||
939 catgtaccttcattctgctcagaaagaaactgattatggaaagaa 988
|||||
301 thrlieCysGluSerSerGllyletrpserasnproserProleCys 317
|||||
989 accatttggaaatcatcactggaatctggtcgaatccagaccatatt 1038
|||||
317 nlylsleuasnplysSerPheserMetilelysgluylaspyrAsnPro 334
|||||
1039 aaaaattggcaaaaagtttctcaatgatttaagcaggtgatttaacccc 1088
|||||
334 eupheleleprovalalavalevalthrAlaPheserGllyleuAla 350
|||||
1089 tcttatttcagtaggcagatcattgattgatttctggtggtgatt 1138
|||||
351 llelletrpLeuAlaArgArgleuLysGlyLysLysSerLysArgSe 367
|||||
1139 atcatttggctggcagaaagagatttaaaaaaagcagaatccaaag 1188
|||||
367 rmetasnAspprotyr 372
|||||
1189 tatgaattgacccattat 1204
|||||

seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT.T14723
seq_documentation_block:
ID T14723 standard: cDNA, 2350 BP.
XX
XX T14723;
AC
AC
DT 31-OCT-1996 (first entry)
XX
DE Human Leu8 antigen cDNA (major transcript).
XX
XX Cell surface antigen: cloning; immunoselection; immunotherapy;
KW therapy; diagnosis; vector; COS; Leu9; T-lymphocyte; ss.
XX
XX Homo sapiens.
XX
XX key Location/Qualifiers
FH CDS 50..1207
FT /*tag= a
FT misc_feature 1079..1514

```





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889 ACCATTGTCGATCATCTGGAATCTGTCGAATCTAGTCAATATGTCA 1038
317 nlyslLeuAspLysSerPheSerMetIleuysgluysaPTyrAsnProL 334
1039 AAAATTGGACAAAAAGTTTCTCATGATTAAGAGGGGTGATTAAACCCCC 1088
334 eupheilleProValAlaValMetValThrAlaPheSerIleuLeuAlaPhe 350
1089 TCCTCATTCACAGTCAGTCATGTTACTGCATTCCTCTGGGTTGCATTT 1138
351 IleIleTripleuAlaArgArgIleuysgluysgluysSerLysArgSce 367
1139 ATCATTTGGCTGGCAAGAGATTAAAAAGCAAGAAATCCAGAGAG 1188
367 rMetAsnAspProTyr 372
1189 TATGAATGACCCCATAT 1204

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seq\_name: /cgn2\_2/gcgdata/geneseq/geneseqn/NA1999.DAT:V81217

seq\_documentation\_block:

ID V81217 standard; CDNA: 2350 BP.

XX V81217;

XX 10-MAY-1999 (first entry)

XX Human Leu8 antigen cDNA.

XX Leu8: cell surface antigen; human; T lymphocyte; CDNA library;

XX ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 50..1207

XX US5849898-A. /\*tag= a

XX 15-DEC-1998.

XX 07-JUN-1995; 95US-0485447.

XX 01-DEC-1992; 92US-0983647.

XX 25-FEB-1988; 88US-0160416.

XX 13-JUL-1989; 89US-0379076.

XX 23-MAR-1990; 90US-0498809.

XX 13-JUL-1990; 90US-0553759.

XX 07-JUN-1995; 95US-0485447.

XX (GENO ) GEN HOSPITAL CORP.

XX Allen J, Amiot M, Aruffo A, Camerini D, Lauffer L;

XX Oquendo C, Seed B, Simmons D, Stamenkovic I, Stengelin S;

XX WPI: 1999-069813/06.

XX P-RSDB: W86199.

XX Example 14; Column 67-70; 79pp; English.

CC This nucleotide sequence comprises human Leu8 cDNA. The cDNA was isolated from a human T lymphocyte cDNA library using a novel method for cloning cDNAs from mammalian expression libraries. The method is based on transient expression of an antigen in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to an antibody-coated substrate. The method is useful for the isolation and molecular cloning of any protein which can be expressed and transported to the cell surface membrane of a

CC eukaryotic cell. It has been used to clone genes (see V81198-220) encoding cell surface antigens such as CD1a, CD1b, CD1c, CD2, CD6, CC CD7, CD13, CD14, CD16, CD19, CD20, CD22, CD26, CD27, CD28, CD31, CC CDw32a, CDw32b, CD33, CD34, CD36, CD37, CD38, CD39, CD40, CD43, CC CD44, CD55, ICAM, LFA-3, FCRII, FCRIIb, T113a and Leu8 (see CC W86188-62, W89151-52 and W88451). CD40 cDNA (see V81198) is CC specifically claimed. Leu8, a T lymphocyte antigen, has been CC expressed in COS cells.

XX Sequence 2350 BP: 679 A; 521 C; 489 G; 661 T; 0 other;

alignment\_scores:

Quality:	Length:
Ratio: 2082.00	372
Percent Similarity: 99.462	Gaps: 0
Percent Identity: 98.656	

alignment\_block:

US-09-119-209-2 x V81217 ..

Align seg 1/1 to: V81217 from: 1 to: 2350

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1 MetIlePheProTyrPlyCysGlnSerThrGlnArgAspLeuTrpAsnI1 17
|||||
89 ATGATATTTCATCGAATGGAATGTGACAGACCCAGAGGACTTATGAAACAT 138
17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHis 34
|||||
139 CTTCAAGTTGTGGGGGTGGACAAATGCTGTGTGATTCCTTGCCACATC 188
34 LSGlyThrTyrcysTrpThrTyHisTyrSerGluLysProMetAsnTrp 50
|||||
189 ATGGAACCGACTGCTGGATACCATTATTCGAAAAACCCATGAACTGG 238
51 GlnArgAlaArgArgPheCysArgAspAsnTrpThrAspLeuValAla1 67
|||||
239 CAAAGGCGTAGAAGATTCTGCCAGACATTACACGATTTAGTGGCAT 288
67 eGlnAsnLysAlaGluIleGluTyrLeuGluLysThrLeuProPheSerA 84
|||||
289 ACAAAACAAAGCGGAAATGAGATCTGAGAGAACTGCTTCCTTCACATC 338
84 rGserTyrTyrTrpIleGlyIleArgLysIleGlyLysIleTrpTrp 100
|||||
339 GTTCTTACTACTAGTAGAATCCGAGAGATGAGAGAAATGACGCTGG 388
101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAspG1 117
|||||
389 GTGGGAACCAACAAATCTCTCAGTGAAGACGAGAACTGGGAGATGG 438
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTrpIle1 134
|||||
439 TGAGCCCAACAAAGAAAGAACAGAGAGAGCTGGTGAATCATATATCA 488
134 yArgAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
|||||
489 AGAGAACAAGATGACAGCAAAATGAGAACGATGACGCTGCCACAAACTA 538
151 LysAlaAlaLeuCysTyrThrAlaSerCysGlnProTrpSerCysSerG1 167
|||||
539 AAGGACGCTCTGTGTACACAGCTTCTTGGCAGCCCTGCGATGACAGTGG 588
167 yHisGlyLysCysValGluIleIleAsnAsnHisThrCysAsnCysAspY 184
|||||
589 CCATGAGAGAATGTAGAAATCATATATTTACACTTGCACACTGTGATGG 638
184 aGlyTyrTyrglyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
|||||
639 TGGGCTACTATGGGCCCCAGTGTGATGTGATCATGAGTGCACCTTTGG 688
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
|||||
689 GAGGCCCAAGAGCTGGGTACCATGAGTACTACTCTTTGGAAACTT 738

```

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217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuT 234
      |||
739 CAGCTTCACGTCACAGTGTGCTTCACTGCTCTGAAGCAAACTTAA 788
      |||
234 hncGlyLeuGluGlnThrThrCysGlyProPheGlyAsnTrpSerSerPro 250
      |||
789 CTGGGATTTGAAGAAACCACTGTGGACCATTTGGAAACTGGTCATCTCCA 838
      |||
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
      |||
839 GAACCACTGTCACGTCATTCAGTGTGAGCCCTCTATTCAGCCACCAATTT 888
      |||
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSera 284
      |||
889 GGGGATCATGAACGTGATGCCATCCCTGGCCAGACTTACGTTACCTCG 938
      |||
284 lAcysThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLysLys 300
      |||
939 CATGTCCTTCATCTGCTCAGAAGCAACTGATTAATGGGAAGAA 988
      |||
301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG 317
      |||
989 ACCATTTGGAATCATCTGAACTGTGCAAACTCCTAGTCCAATATGTCA 1038
      |||
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTrpAsnPro 334
      |||
1039 AAATTTGGCAAAAGTTTCTCATGTATTAAGAGGGTGATTAACCC 1088
      |||
334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
      |||
1089 TCTTCATTCACAGTCGAGTCATGCTTACCTGCTGCTGGCATTTT 1138
      |||
351 IleIleTrpLeuAlaArgLeuLysLysGlyLysLysSerLysArgSe 367
      |||
1139 ATCATTTGGCTGGCAAGAGATTAAAAAAGCAAGAAATCCAAAGAGAG 1188
      |||
367 rMetAsnAspProTyr 372
      |||
1189 TATGATGACCCATAT 1204

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seq\_name: /cgn2\_2/gcndata/geneseq/geneseq/NA1993.DAT.038839

seq\_documentation\_block:

ID Q38839 standard: cDNA: 2330 BP.

AC Q38839:

XX 17-AUG-1993 (first entry)

XX Sequence of LAM-1 cDNA.

XX Leukocyte adhesion molecule-1, lymphocyte-associated molecule-1;

KM LAM-1; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 53..1210

FT /\*tag= a

XX MO9306835-A.

XX 15-APR-1993.

XX 05-OCT-1992; 92WO-2008467.

XX 03-OCT-1991; 91US-0770608.

XX (DAND ) DANA FARBER CANCER INST INC.

XX Tedder TF, Spertini OG;

```

DR WPI: 1993-134119/16.
DR P-PSDB: R34197.
XX
PT Detection of inflammation or disease site - by using labelled
PT Leukocyte adhesion molecule-1 - treats leukocyte-mobilising
PT conditions, auto-immune disorders, cancer etc.
XX
PS Disclosure: Fig 2; 44pp; English.
XX
CC cDNA encoding the LAM-1 protein was isolated from a human tonsil
CC cDNA library (ATCC 37546). The mature LAM-1 protein has an
CC extracellular region of about 294 amino acids containing 7 potential
CC N-linked carbohydrate attachment sites. LAM-1 has a cytoplasmic tail
CC of 17 amino acids containing 8 basic and 1 acidic residues. The
CC processed LAM-1 protein has a Mr of at least 50,000. LAM-1 combines
CC domains homologous to domains found in three distinct families of
CC molecules: animal lectins, growth factors, and C3/C4 binding proteins.
XX
SQ Sequence 2330 BP; 661 A; 527 C; 482 G; 660 T; 0 other:

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alignment\_scores: Quality: 2076.00 Length: 372  
Ratio: 5.611 Gaps: 0  
Percent Similarity: 99.462 Percent Identity: 98.118

alignment\_block: US-09-119-209-2 x Q38839 ..

Align seg 1/1 to: Q38839 from: 1 to: 2330

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1 MetIlePheProTrpPlyscysGlnSerThrGlnArgAspLeuTrpAsnI 17
      |||
92 ATATATTTTCATGGAATATGTCGAGACACCCAGAGGACTTATGAAACAT 141
      |||
17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHis 34
      |||
142 CTTCAGATTGTGGGGGTGAGACATGCTCTGTGTGATTTCTCGGCACATC 191
      |||
34 lAsGlyThrTrpCysTrpThrTrpHisTyrSerGluLysProMetAsnTrp 50
      |||
192 ATGGAACCGACGCTGACTTACCATTAATTCGAAAAACCCAGAACTGCG 241
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 : Patent No. 5679346  
 : GENERAL INFORMATION:  
 : APPLICANT: Tedder, Thomas F. and Olivier G. Sperl  
 : TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYTE-ASSOCIATED CELL  
 : NUMBER OF SEQUENCES: 1  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: FISH & NEAVE  
 : STREET: 1251 Avenue of the Americas  
 : CITY: New York  
 : STATE: NY  
 : COUNTRY: USA  
 : ZIP: 10020  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.25  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/481,803  
 : FILING DATE:  
 : CLASSIFICATION: 424  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/215,366  
 : FILING DATE: 21-MAR-1994  
 : APPLICATION NUMBER: US 07/720,602  
 : FILING DATE: 25-JUN-1991  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 07/313,109  
 : FILING DATE: 21-FEB-1989  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: James F. Haley, Jr.  
 : REGISTRATION NUMBER: 27,794  
 : REFERENCE/DOCKET NUMBER: CG-101 CON  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (212) 596-9000  
 : TELEFAX: (212) 596-9090  
 : TELEX:  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 2330 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : HYPOTHEICAL: NO  
 : ANTI-SENSE: NO  
 : FEATURE:  
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 : LOCATION: 53..1210  
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: Patent No. 576775
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: GENERAL INFORMATION:
: APPLICANT: Tedder, Thomas F. and Olivier G. Sperlin
: TITLE OF INVENTION: MONOCLONAL ANTIBODY TO LYMPHOCYNE-ASSOCIATED
: NUMBER OF SEQUENCES: 1
: CORRESPONDENCE ADDRESS:
: ADDRESS: WHITE & CASE
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/215,366A
: FILING DATE: 21-MAR-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/720,602
: FILING DATE: 25-JUN-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/313,109
: FILING DATE: 21-FEB-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Neils T. Lipsett
: REGISTRATION NUMBER: 25,888
: REFERENCE/DOCKET NUMBER: 1110684-0005
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 819-8582
: TELEFAX: (212) 354-8113
: TELEX:
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: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2330 base pairs
: TYPE: nucleic acid

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TOPOLOGY: linear
MOLECULE TYPE: cDNA
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; Patent No. 5808025
; GENERAL INFORMATION:
; APPLICANT: Teoder, Thomas F.
; TITLE OF INVENTION: KANSAS, Geoffrey S.
; TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,539A
; FILING DATE: 16-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,459
; FILING DATE: 25-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gunnison, Jane
; REGISTRATION NUMBER: 38,479

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TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2330 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
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642 TGGGGTACTATGAGCCGCCAGTGTCACTTTTGATTCAGTGTGACCCCTTGG 691  
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsn 217  
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692 GAGGCCCCAGAGCTGGGTACCATGACTTACTACACCTTTGGAAACTT 741  
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeu 234  
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742 CAAGCTCAACCTCAGAGTGTGCTTCAAGTGTCTGTGAGGAAACAACCTTAA 791  
234 hGlyIleGluGluThrThrCysGlyProPheGlyAsnTrpSerSerPro 250  
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792 CTGGGATTTGAAGAAACACACCTGTGAACCATTTGGAAACTGTCTCATCTCCA 841  
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAsp 267  
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842 GAACCAACCTGTCAAGTGAATTCAGTGTGAGCTCTATTCAGCACCCAGATT 891  
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSerA 284  
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892 GGGATCATGAACTGATGACATCCCTGGCCAGCTTCACCTTACTCTGTG 941  
284 IacysThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300  
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942 CATGTACCTTCATCTGCTCAGAAAGAACTGACTTAATTGGAAAGAAA 991  
301 ThrIleCysGluSerSerGlyTrpSerAsnProSerProIleCysG 317  
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992 ACCATTGTGAATCATCTGGAATCTGGTCAAAATCCATGACCAATATGTCA 1041  
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrrAsnPro 334  
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1042 AAAATTGGACAAGATTTCTCAATGATTAAGAGAGGTGATTTAAACCCC 1091  
334 eUpheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350  
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1092 TCTTCATTTCCAGTGGCAGCATGATGTTACTGCAATCTCTGGTGGCATATT 1141  
351 IleIleTrpLeuAlaArgArgLeuLysGlyLysLysSerLysArgSe 367  
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1142 ATCATTTGGCTGGCAAGAGATTAATAAAGCAAGAAATCCAAAGAGAAG 1191  
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seq\_documentation\_block:  
Sequence 1, Application US/08461592B  
Patent No. 5834425  
GENERAL INFORMATION:  
APPLICANT: Tedder, Thomas F.  
APPLICANT: Kansas, Geoffrey S.  
TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes  
STREET: Ten Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,592B  
FILING DATE:  
CLASSIFICATION: 514

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/340,539
FILING DATE: 16-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,459
FILING DATE: 25-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: CG-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 53..1210
US-08-461-592B-1

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Ratio: 5.611          Gaps: 0
Percent Similarity: 99.462      Percent Identity: 98.118

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142 CTTCAGATTGTGGGGTGGACATGCTGCTGTGATTTCTGGCACATC 191
34 IsGlyThrTrpCysTrpThrTrpHisTrpSerGluLysProMetAsnTrp 50
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192 ATGGAACCCAGCTGCTGACTTACCATTTATTCGAAACCACATGAACTGG 241
51 GlnArgAlaIaArgArgPheCysArgAspAsnTrpThrAspLeuValAla11 67
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242 CAAAGGCGCTAGAAATTTCTGCCGAGACAAATTACACAGATTAGTTGCCAT 291
67 eGlnAsnLysAlaGluIleGluTrpLeuGluLysThrLeuProPheSerA 84
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292 ACAAACAAGCGGGAATTGAGTATCTGGAAGAAGACTGCTGCTTTCAGTC 341
84 rGSerTrpTrpTrpIleGlyIleArgLysIleGlyGlyIleTrpThrTrp 100
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342 GTTCTTACTACTGATAGGAATCCGGAAGATAGAGGAAATATGAGCGTGG 391
101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAspG1 117
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117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTrpIleL 134
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442 TGAGCCCAACAACAAGAAAGACAGAGGAGCTGGGTGGAATCATATCA 491
134 ySArgAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
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492 AGAACAACAAGATCGAGCGAAATGGAACGATGACGCTGCCACAACCTA 541
151 LysAlaAlaLeuCyScysTrpThrAlaSerCySglnProTrpSerCySserG1 167
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167 yHisGlyGluCysValGluIleIleAsnAsnHisThrCysAsnCysAspV 184
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592 CCATGAGATATGTAGAAATCATCAATTAATTAACCGCAACTGTGATG 641
184 aGlyTrpTrpGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
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642 TGGGGTACTATGCGCCCAAGTCTCAGTTTGATTCAGTGTGAGCCCTTGG 691
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
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692 GAGGCCCAAGAGCTGGGATCAGTACGAGTACCTGACCTTTGGGAACCTT 741
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742 CACTTCAACTACAGTGTGCTTACCTGCTGCTGGAAGAACTTAA 791
234 hrgIyIleGluGluThrTrpCysGlyProPheGlyAsnTrpSerSerPro 250
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792 CTGGGATTGAGAAGAACCACTGCTGAACCATTTGGAACCTGTATCTCCA 841
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
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842 GAAACAACCTGTCAAGTATTCAGTGTGAGCCCTTATCAGACACCAATTT 891
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892 GGGATCATGACCTGTAGCCATCCCTGGCCACCTTACGCTTACCTCTG 941
284 lAcysThrPheIleCysSerGlyThrGluLeuIleGlyLysLysLys 300
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942 CATGTACCTTCATCTGCTCAGAAAGAACTGATTATGGAAGAAGAA 991
301 ThrIleCysGlnSerSerGlyIleTrpSerAsnProSerProIleCysG1 317
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992 ACCATTGTGTAATCATCTGGAATCTGTGCAAAATCTCAAGTCCAATATGCA 1041
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTrpAsnProL 334
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1042 AAATTGGACAAAAGTTTCTCAATGATTTAAGGAGGTGATTTAACCCCC 1091
334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
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1092 TCTTCATTTCCAGTGGCAATCATGTTACTGCAATCTCTGGGTGGCATTT 1141
351 IleIleTrpLeuAlaIaArgArgLeuLysLysGlyLysSerLysArgSe 367
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367 rMetAsnAspProTrp 372
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1192 TATGATGACCCATAT 1207

seq_name: /cgn2_6/ptodata/2/lna/backfile1.seq:5514582-1
seq_documentation_block:
PATENT NO. 5514582
APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,670
FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
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; FILING DATE: 16-DEC-1991
; APPLICATION NUMBER: 440, 625
; FILING DATE: 22-NOV-1989
; APPLICATION NUMBER: 315, 015
; FILING DATE: 23-FEB-1989
; SEQ ID NO: 1:
; LENGTH: 1829
5514582-1

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  Ratio: 5.607          Gaps: 1
Percent Similarity: 98.925 Percent Identity: 98.656

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alignment_block:
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17 ePheLysLeuTrpGlyTrpThrMetLeuScySAspPheLeuAlaHis 34
  |||||||
179 CTTCAGATTGTGGGGGTGGACATGCTCTGTGTGATTTCCGTGGCAATC 228
34 IsGlyThrTyrcysTrpThrTyrrHisTyrSerGluLysProMetAsnTrp 50
  |||||||
229 ATGGAACCTACTGCTGACTTACCATTTATTCGAAAAACCATGAACGTG 278
51 GlnArgAlaArgArgPheCysArgAspAsnTyrrThrAspLeuValAlaIle 67
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279 CAAGGGCTGAGAGATTGTGCCGAGACAATTACACAGATTTAGTTGCCAT 328
67 eGlnAsnLysAlaGluIleGluTyrLeuGluLysThrLeuProPheSerA 84
  |||||||
329 ACAAAACAAGCCCGAATTGAGATCTGAGAAAGACTCTGCCCTTCAGTC 378
84 rGSerTyrrTyrrTrpIleGlyIleArgLysIleGlyIleTrpThrTrp 100
  |||||||
379 GTTCTTACTACTGATGAGATCCGGAGATGAGAGAAATATGACGTG 428
101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAspG 117
  |||||||
429 GTGGGAACCAACAATCTCTCACTGAAGACGACAGAACTGGGAGATG 478
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIle 134
  |||||||
479 TGAGCCCAACACACAGACAGACAGACAGACAGACAGACAGACAGACAG 528
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579 AAGGCAGCCCTCTGTACACACCTTCTTCCAGCCCTGTGTCATGCGAGT 628
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629 CCATGGAGAAATGTGTAGAATCATCAATATCACACCTCCAACTGTGATG 678
184 aGlyTyrrTyrrGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
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679 TGGGGTACTATGAGCCCGCAGTGTACCTGTGATTCAGTGTGAGCTTTG 728
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
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779 CAGCTCAGCTCACAGTGTGCTTCACTGCTGAGGAACAACCTAA 828
234 hrcGlyIleGluGluThrThrCysGlyProPheGlyLysnTrpSerSerPro 250
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829 CTGGGATTGAAGAAACCACTGTGGACCAATTGTGAACTGTATCTCCA 878
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
  |||||||
879 GAACCAACCTCTAG.....TGTGACCTCTATCAGCACCAATTT 918
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSerA 284
  |||||||
919 GGGGATCATGAAGTATGACCATCCCTGGCCACTTACAGTCTTACCTCG 968
284 IacysThrPheIleCysSerGlyGlyThrGluLeuIleGlyLysLysLys 300
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969 CATGTACCTTCATCTGCTCAGAGGAACGTGTAATTGGGAAGAGAAA 1018
301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG 317
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317 nLysLeuAspLysSerPheSerMetIleLysGlyGlyAspTyrrAsnProL 334
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334 eUpheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
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1119 TCTTCATTCAGTGGCAGTCATGTTACTGCAATTCCTGGTGGCATTT 1168
351 IleIleTrpLeuAlaArgArgLeuLysGlyLysLysSerLysArgSe 367
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; Sequence 3, Application US/08513278
; Patent No. 5840844
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: STACHELL, SCOTT E.
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: SINGER, MARK S.
; APPLICANT: YEDNOCK, TED A.
; TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,278
; FILING DATE: 10-AUG-1995
; CLASSIFICATION: 5530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059027
; FILING DATE: 06-MAY-1993
; APPLICATION NUMBER: 07/786149
; FILING DATE: 31-OCT-1991

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/315015
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET INFORMATION: 565D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2214 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-513-278-3
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## alignment block:

US-09-119-209-2 x US-08-513-278-3 ..

Align seg 1/1 to: US-08-513-278-3 from: 1 to: 2214

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356 CTATTATACACTGATGAGATCAGAAATTCGGAATAATTCGGACATGG 405
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406 GTGGGAACCAACAAACTCTCACTAAGACAGAGAACTGGGGTGGCTGG 455
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506 AGAGGAAGAGAGACTGTGGAAATGAGATGACGCTGTGCACAAACGA 555
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151 LysAlaIleLeuCyScyTrpThrAlaSerCysGlnProTrpSerCysSer 167
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184 aLgLyTrpTyrGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
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seq_name: /cgn2_6/ptodata/2/ina/backfiles1.seq:5514582-3
seq_documentation_block:
; Patent No: 5514582
; APPLICANT: CAPON, DANIEL J.; TASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
; IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 43
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-08/185,670
; FILING DATE: 21-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 986,931
; FILING DATE: 08-DEC-1992
; APPLICATION NUMBER: 808,122
; FILING DATE: 16-DEC-1991
; APPLICATION NUMBER: 440,625
; FILING DATE: 22-NOV-1989
; APPLICATION NUMBER: 315,015
; FILING DATE: 23-FEB-1989
; SEQ ID NO: 3
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5514582-3
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SYNOPSIS AND CONCLUSION: /note= "potential polyadenylation



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: OTHER INFORMATION: signals"
:
: FEATURE:
: NAME/KEY: polyA-signal
: LOCATION: 3124..3130
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PCT-US91-05059-1

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alignment block:  
US-09-119-209-2 x PCT-US91-05059-1 ..

Align seg 1/1 to: PCT-US91-05059-1 from: 1 to: 3144

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      11 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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      58 ArgAspAsnTrpThrAspLeuValAlaIleGlnAsnLysAlaGluIleG 74
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      219 CAGAAATCCGTACACAGACTTACTGGCCATCCAGATMAAATGAATATCA 268
      74 uTyrLeuGluYsThrLeuProPheSerArgSerTrpTrpIleGlyI 91
      11 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      269 TTACCTCAATAGTCTCTACCTACTACAGCTCTACTACTGATGGAGA 318
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      369 ACCAAGACGACCTGACAGACTGGCTGATATGAACTTAACAAAGAAAGGA 418
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      11 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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      141 yStrAsnAspAspAlaCysHisLysLeuLysAlaAlaLeuCysTrpTrh 157
      11 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      469 AGTGAATGATGAGCATGCTTGAAGAAAGAACGACGATTTGGTTACACA 518
      158 AlaSerCysGlnProTrpSerCysSerGlyHisGlyGluCysValGluI 174
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719 CTTCACATGCACTGACGGGTACCACTAAATAGGCCCCACAGCACTGGAA 768
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seq_name: /cgn2_6/prodata/2/ina/5A_COMB.seq:US-08-365-470-2
seq_documentation_block:
: Sequence 2, Application US/08365470
: Patent No. 5632991
: GENERAL INFORMATION:
: APPLICANT: Gimprone, Jr., Michael A.
: TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX
: STREET: 1100 New York Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/365,470
: FILING DATE: herewith
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/102,510
: FILING DATE: 05-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/850,802
: FILING DATE: 13-MAR-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Markowicz, Karen R.
: REGISTRATION NUMBER: 36,351
: REFERENCE/DOCKET NUMBER: 0627.1350003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2540
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1833 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: nucleic acid
: LOCATION: 1-1833
: OTHER INFORMATION: /label = nucleic acid
: OTHER INFORMATION: /note = SEQ ID NO:2 begins at base pair position 117 and e
: OTHER INFORMATION: base pair position 1949.

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US-08-365-470-2

alignment\_scores:  
 Quality: 862.00 Length: 279  
 Ratio: 3.883 Gaps: 0  
 Percent Similarity: 79.570 Percent Identity: 51.971

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Align seg 1/1 to: US-08-365-470-2 from: 1 to: 1833

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seq\_documentation\_block:

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: Sequence 18, Application US/09209668A
: Patent No. 6114517
: GENERAL INFORMATION:
: APPLICANT: Monia, Bret P.
: APPLICANT: Xu, Xiaoxing S.
: TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
: TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES
: FILE REFERENCE: ISPH-0336
: CURRENT APPLICATION NUMBER: US/09/209,668A
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 18
: LENGTH: 3834
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (117)..(1949)
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: M24736/genbank
: DATABASE ENTRY DATE: 1994-11-07
US-09-209-668-18

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Quality: 862.00 Length: 279  
 Ratio: 3.883 Gaps: 0  
 Percent Similarity: 79.570 Percent Identity: 51.971

alignment\_block:

US-09-119-209-2 x US-09-209-668-18 ..

Align seg 1/1 to: US-09-209-668-18 from: 1 to: 3834

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: Sequence 1, Application US/08365470
: Patent No. 5632991
: GENERAL INFORMATION:
: APPLICANT: Gimprone, Jr., Michael A.
: TITLE OF INVENTION: Antibodies Specific For E-selectin And The Uses
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX
: STREET: 1100 New York Ave., NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/365,470
: FILING DATE: herewith
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/102,510
: FILING DATE: 05-AUG-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/850,802
: FILING DATE: 13-MAR-1992

```

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: ATTORNEY/AGENT INFORMATION:
: NAME: Markowicz, Karen R.
: REGISTRATION NUMBER: 36,351
: REFERENCE/DOCKET NUMBER: 0627.1350003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3854 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-365-470-1

alignment_scores:
Quality: 862.00 Length: 279
Ratio: 3.883 Gaps: 0
Percent Similarity: 79.570 Percent Identity: 51.971

alignment_block:
US-09-119-209-2 x US-08-365-470-1 ..
Align seg 1/1 to: US-08-365-470-1 from: 1 to: 3854

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122 yLysAsnLysGluAspCysValGluIleTyrIleLysArgAsnLysAsp 138
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480 GTGGGATGTGCAATGATGAGAGTGCACACAAAGAACTTGCCTATAG 529
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; Patent No. 5883082

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; GENERAL INFORMATION:

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; APPLICANT: Bennett and Stepkowski

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; TITLE OF INVENTION: Compositions and Methods for Preventing

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; NUMBER OF INVENTION: and Treating Allotraft Rejection

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; CORRESPONDENCE ADDRESS:

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; ADDRESSEE: Woodland Falls Corporate Park

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; STREET: 210 Lake Drive East, Suite 201

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; CITY: Cherry Hill

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; STATE: NJ

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; COUNTRY: USA

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; ZIP: 08002

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; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

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; COMPUTER: IBM PS/2

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; OPERATING SYSTEM: PC-DOS

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; SOFTWARE: WORDPERFECT 5.0

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; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/344,155C

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; FILING DATE: No. 5883082ember 23, 1994

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; CLASSIFICATION: 514

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; PRIOR APPLICATION DATA:

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; FILING DATE: September 2, 1992

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; PRIOR APPLICATION NUMBER: PCT/US91/05209

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; FILING DATE: July 23, 1991

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/063,167

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; FILING DATE: 5/17/93

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 08/007,997

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; FILING DATE: 1/21/93

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/939,855

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; FILING DATE: 9/2/92

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 07/567,286

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; FILING DATE: 8/14/90

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; ATTORNEY/AGENT INFORMATION:

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; NAME: Jane Massey Licata

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; REGISTRATION NUMBER: 32,257

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```

; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (609) 779-2400

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; TELEFAX: (609) 779-8488

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; INFORMATION FOR SEQ ID NO: 98:

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; SEQUENCE CHARACTERISTICS:
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; LENGTH: 3858
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: No
US-08-344-155C-98

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    Percent Similarity: 79.570      Percent Identity: 51.971

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alignment_block:
US-09-119-209-2 x US-08-344-155C-98

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55 gPheCysArgAspAsnTyrThrAspLeuValAlaIleGlnAsnLysAla 72
    |||
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72 LuIleGluTyrLeuGluLysThrLeuProPheSerArgSerTyrTyrTrp 88
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122 yLysAsnLysGluAspCysValGluIleTyrIleLysArgAsnLysAsp 138
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    |||
139 AlaGlyLysTrpAsnAspAspAlaCysHisLysLeuValAlaAlaLeu 155
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    |||
155 sTyrThrAlaSerCysGlnProTrpSerCysSerLysLysGlyGlyCys 172
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    |||
604 TAGAGACCATCAATTAATTAACCTTGAAGTGGACCTGGCTGAGTGA 653
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189 ProGlnCysGlnLeuValIleGlnCysGluProLeuGluAlaProGlu 205
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654 CTCAACTGTGACCAAAATGTGAACTGTACAGCCCTGGAATCCCTGAGCA 703
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704 CTGCTCTATCAGCTGTATGAGGCTTACCTGCCAAGACACACATGAGACC 803
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222 InCysAlaPheSerCysSerGluGlyThrAsnLeuThrGlyIleGlu 238
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754 CCGTCTATCAGCTGTATGAGGCTTACCTGCCAAGACACACATGAGACC 803
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239 ThrThrCysGlyProPheGlyAsnTrpSerSerProGluProThrCys 255
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804 ATGACGTATATGCTCTGTGAGAAATGAGTGTCTATTCACCACTGGCAA 853
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904 GTTCCAAAACCTGTGAGCTTCCCATGTGACACAACTGTACATTGAC 953
289 CysSerGluGlyThrGluLeuIleGlyLysLysLysThrIleCysGlu 305
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seq_documentation_block:
; Patent No. 5217870
; APPLICANT: HESSTON, CATHERINE A.; LOBB, ROY R.; GOELZ, SUSAN E.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST CDX
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/345,151
; FILING DATE: 28-APR-1989
; SEQ ID NO:1
; LENGTH: 3863
5217870-1

alignment_scores:
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254 TTATGTGTGCAAAAGGTACACACCTGTTGCAATTCAAAACAAAGAAG 303
72 IuIleGluTYrLeuGluYsThrLeuProPheSerArgSerTYrTYrTrp 88
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139 AlaGlyLysTrpAsnAspAspAlaCysHisLysLeuLysAlaAlaLeu 155
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654 CTGAATGTGAGCAATTTGGAACCTGTACAGCCCTGGAAATCCCTTAGCA 703
205 uGlyTrpMetAspCysThrHisProPheGlyAsnPheSerPheSerSerc 222
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239 ThrThrCysGlyProPheGlyAsnTrpSerSerProGluProThrCysG 255
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854 TGTGTTGAGTGTGATGTGTGACAAATCCAGCAATGGGTTGCTGGAAAT 903
272 ysserHisProLeuAlaSerPheSerPheThrSerAlaCysThrPheIle 288
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904 GTTCCAAAACCTCGGAAGCTTCCCATGTGAAACACAACCTGTACATTGTGAC 953
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Date: Jan 13, 2001 3:39 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

## Command line parameters:

-MODEL=frame+pn.model -DEV=xlp  
-O=/cgn2\_1/USPTO.spool/US09119209/runat.08012001.083825.2022/app\_query.fasta\_1.434  
-DB=Pending\_Patents\_NA -OPMT=fastap -SUFFIX=rip -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000  
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blomsum62  
-TRANS=human40.cdi -LIST=45 -DOCALIG=200 -THR SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORFEXT -MINLEN=0 -MAXLEN=200000000  
-USER=US09119209.ecgn1\_1\_4213 -NCPU=6 -ICPU=3 -LONGLOC -NO\_XLPXY  
-WAIT -THREADS=1

## Search Information block:

Query: US-09-119-209-2  
Query Length: 372  
Database: Pending\_Patents\_NA\*  
Database sequences: 12197726  
Database Length: 177387503  
Search time (sec): 1726.500000

## score\_list:

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! APPLICANT: LASKY, LAURENCE A.  
! APPLICANT: STACHELL, SCOTT E.  
! APPLICANT: ROSEN, STEVEN D.  
! APPLICANT: SINGER, MARK S.  
! APPLICANT: YEDNICK, TED A.  
! TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS  
! NUMBER OF SEQUENCES: 6  
! CORRESPONDENCE ADDRESS:  
! STREET: 1 DNA Way  
! CITY: South San Francisco  
! STATE: California  
! COUNTRY: USA  
! ZIP: 94080  
! COMPUTER READABLE FORM:  
! MEDIUM TYPE: 3.5 inch, 1.44 Mb Floppy disk  
! OPERATING SYSTEM: IBM PC compatible  
! SOFTWARE: WinPatIn (Genentech)  
! CURRENT APPLICATION DATA:  
! APPLICATION NUMBER: US/09/119,209  
! FILING DATE: 20-Jul-1998  
! CLASSIFICATION:  
! PRIOR APPLICATION DATA:  
! APPLICATION NUMBER: 08/513278  
! FILING DATE: 10-AUG-1995  
! PRIOR APPLICATION DATA:  
! APPLICATION NUMBER: 08/059027  
! FILING DATE: 6-MAY-1993  
! PRIOR APPLICATION DATA:  
! APPLICATION NUMBER: 07/786149  
! FILING DATE: 31-OCT-1991  
! PRIOR APPLICATION DATA:  
! APPLICATION NUMBER: 07/315015  
! FILING DATE: 23-FEB-1989  
! ATTORNEY/AGENT INFORMATION:  
! NAME: Love, Richard B.  
! REGISTRATION NUMBER: 34,659  
! REFERENCE/DOCKET NUMBER: P0565D1C3  
! TELECOMMUNICATION INFORMATION:  
! TELEPHONE: 650/225-5530  
! TELEFAX: 650/952-9881  
! INFORMATION FOR SEQ ID NO: 1:  
! SEQUENCE CHARACTERISTICS:  
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! TOPOLOGY: Linear  
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seq\_documentation block:

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: Sequence 1154, Application US/09023655
: GENERAL INFORMATION:
: APPLICANT: Cocks, Benjamin G.
: APPLICANT: Susan G. Stuart
: APPLICANT: Jeffrey J. Seilhamer
: TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
: NUMBER OF SEQUENCES: 1508
: CORRESPONDENCE ADDRESS:
: ADDRESS: INCYTE PHARMACEUTICALS, INC.
: STREET: 3174 PORTER DRIVE
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/023.655
: FILING DATE: HERewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Zeller, Karen J.
: REGISTRATION NUMBER: 37, 071
: REFERENCE/DOCKET NUMBER: PA-0001 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 855-0555
: TELEFAX: (650) 845-4166
: INFORMATION FOR SEQ ID NO: 1154:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2354 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GENBANK
: CLONE: 9187182
US-09-023-655-1154

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alignment\_scores:

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Quality: 2094.00 Length: 372
Ratio: 5.644 Gaps: 0
Percent Similarity: 99.731 Percent Identity: 99.194

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alignment\_block:  
US-09-119-209-2 x US-09-023-655-1154 ..

Align seg 1/1 to: US-09-023-655-1154 from: 1 to: 2354

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17 ePheLysLeuTrpGlyTrpThrMetLeuCysAspPheLeuAlaHisH 34
  |||
166 CTTCACAGTTGTGGGGGTGGACAATGCTCTGTGTGATTTCTGGCACATC 215
34 IsGlyThrTyrcysTrpThrTyHIsTySerGluLysProMetAsnTrp 50
  |||
216 ATGGAACGACACTGCTGACTTACCATTTATTCGAATAAACCCATGAACTGG 265
51 GlnArgAlaArgArgPheCysArgAspAsnTyrrThrAspLeuValAlaI1 67
  |||
266 CAACGGCGTAGAAGATTTCTGCCGAGACAATTCACAGATTAGTTGCCCAT 315
67 eGlnAsnLysAlaGluIleGlyTrLeuGluLysThrLeuProPheSerA 84
  |||
316 ACAAACAAGCGCGAATTTGAGTATCTGGAGAAGACTGCGCTTTCAGTTC 365
84 rGSerTyrrTyrrpIleGlyIleArgLysIleGlyGlyTleTrpThrTrp 100
  |||
366 GTTCTTACTACTGATAGAGATCCGGAAGATAGAGAGATATGAGAGCTGG 415
101 ValGlyThrAsnLysSerLeuThrGluAlaGluAsnTrpGlyAspS1 117
  |||
416 GTGGACCAACCAAAATCTTACTGAAAGCAGACAACCTGGGAGATG 465
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrrIle1 134
  |||
466 TGAGGCCCAACAACAAGAACAGACAGAGCGCGGAGATCTATATCA 515
134 ySarGAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHIsLysLeu 150
  |||
516 AGAGAAACAAGATGACAGCAATGGAACGATGACCCCTGCCAACAACGTA 565
151 LysAlaAlaLeuCysTyrrThrAlaSerCysGlnProTrpSerCysSerG1 167
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566 AAGCGAGCCCTCTGTACACAGCTTCTTCCAGCCCTGCTCATTCAGTGG 615
167 yHisGlyGluCysValGluIleIleAsnAsnHisThrCysAsnCysAspY 184
  |||
616 CCATGAGAGATGTCAGAAATCATTAATTAACACTGCCAAGCTGTGATG 665
184 aIGlyTyrrGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
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666 TGGGTACTATGGGCCCAAGTGTCAAGCTTGATGATTCAGGTGAGCCCTTGG 715
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
  |||
716 GAGGCCCCAGAGCTGGGTACCATGAGCTGTACTCAACCCCTTGGAAACT 765
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuTr 234
  |||
766 CAGCTTCAGCTCACAGTGTCCCTTCAGCTGTGAGAGAACCAACTTAA 815
234 hrGlyIleGlnGluThrThrCysGlyProPheGlyAsnTrpSerSerPro 250
  |||
816 CTGGGATTGAGAAACCAACCTGTGGACCACTTTGGAAACTGGTCACTCCA 865
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
  |||
866 GAACCAACCTGTCAAGTGTACGTGAGCCCTCATTCAGCACCAAGATT 915
267 uGlyIleMetAsnCysSerHisPProLeuAlaSerPheSerPheThrSerA 284
  |||
916 GGGCATCATGAACCTGTAGCAATCCCTGCCAGCTTCAGCTTACCTCTCG 965

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284 lAcysThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
  |||
966 CATGTACTTCATCTGCTCAGAAAGAACTGAGTTATTTGGAAAGAA 1015
301 ThrIleCysGlnSerSerGlyIleTrpSerAsnProSerProIleCysG1 317
  |||
1016 ACCATTGTGAATCATCTGGAATCTGTGCAAAATCCYAGTCCAAATATGTCA 1065
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrrAsnProL 334
  |||
1066 AAAATTGGACAAAGTTTCTCAATGATTAAGAGGGGTGATTTTAAACCCCC 1115
334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
  |||
1116 TCTTCATTCCAGTGGCAGTCATGTTACTGTCATTCCTCTGGTTGGCATTT 1165
351 IleIleTrpLeuAlaArgArgLeuLysLysGlyLysLysSerLysArgSe 367
  |||
1166 ATCATTTGGCTGGCAAGCAGATTAATAAAAGCAAGAAATCCAAAGAGAG 1215
367 rMetAsnAspProTyrr 372
  |||
1216 TATGAATGACCCCATAT 1231

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seq\_name: /cgn2\_6/ptodata/2/pna/US6021\_COMB.seq:US-60-213-360-1118

seq\_documentation\_block:

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: Sequence 1118, Application US/60213360
: GENERAL INFORMATION:
: APPLICANT: Morris, MacDonald
: APPLICANT: Lal, Preeti
: APPLICANT: Diep, Dinh
: TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
: TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
: FILE REFERENCE: GX-0014 P
: CURRENT APPLICATION NUMBER: US/60/213,360
: CURRENT FILING DATE: 2000-06-21
: NUMBER OF SEQ ID NOS: 8347
: SOFTWARE: PERL Program
: SEQ ID NO 1118
: LENGTH: 2385
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: OTHER INFORMATION: Incyte ID No: 331616.2
US-60-213-360-1118

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alignment\_scores:

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Quality: 2090.00 Length: 372
Ratio: 5.633 Gaps: 0
Percent Similarity: 99.731 Percent Identity: 98.925

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alignment\_block:

US-09-119-209-2 x US-60-213-360-1118 ..

Align seg 1/1 to: US-60-213-360-1118 from: 1 to: 2385

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17 ePheLysLeuTrpGlyTrpThrMetLeuCysAspPheLeuAlaHisH 34
  |||
187 CTTCACAGTTGTGGGGGTGGACAATGCTCTGTGTGATTTCTGGCACATC 236
34 IsGlyThrTyrcysTrpThrTyHIsTySerGluLysProMetAsnTrp 50
  |||
237 ATGGAACGACACTGCTGACTTACCATTTATTCGAATAAACCCATGAACTGG 286
51 GlnArgAlaArgArgPheCysArgAspAsnTyrrThrAspLeuValAlaI1 67

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|||||
287 CAAGGGCTAGAGATCTGCCGAGACAAATTACACAGATTAGTTGGCAT 336
67 eglInsnlysaIaGluIleGluThrLeuGluLysThrLeuProPheSera 84
|||||
337 ACMAAACAGGCGGGAATTGAGTATCTGGAGAAAGACACTGCTTCAGTC 386
84 rgseryTyrTrpIleGlyIleArgLysIleGlyIleTrpThrTrp 100
|||||
387 GTTCTTACTACTGATGAGATCCGGAAGATGAGAGAAATATGACCTGCG 436
101 ValGlyThrAsnLysSerLeuThrGluIuAaGluAsnTrpGlyAspG1 117
|||||
437 GTGGGAACCAACAATCTCTTACTGAAAGACGAGAACTGGGGAGATGG 486
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIleL 134
|||||
487 TGAGCCCAACACAGAAAGAAACAAAGAGAGCTGGTGGAATCTATATCA 536
134 ysaArgAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
|||||
537 AGAGAAACAAAGATGCGAGCAATGGAACGATGACGCTGCCAACATA 586
151 LysAlaIaIaLeuCysTrpThrAlaSerCysGlnProTrpSerCysSerG1 167
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587 AAGGCAACCTCTGTTACACAGCTTCTGCCAGCCTGCTCATGACAGTGG 636
167 yHisGlyGluCysValGluIleIleAsnAsnHisTrpCysAspCysAspY 184
|||||
637 CCATGGAGATGTGTGAATCATCATATATACACCTGCACACTGTGATGG 686
184 aIeGlyTyrTrpGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
|||||
687 TGGGGTACTATGGGCCCACTGTCAGTTGTGATTCAGTGTGAGCCTTGG 736
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnPh 217
|||||
737 GAGGCCCAAGAGTGGGTACCATGACCTACTCACCCCTTTGGAAACTT 786
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuT 234
|||||
787 CAGCTTCACATCAAGTGTGCTCAGTGTGCTGAGAGAACAAACTTAA 836
234 hieGlyIleGluIuThrTrpCysGlyProPheGlyAsnTrpSerSerPro 250
|||||
837 CTGGGATTAAAGAAACACCTGTGAGCAATTTGGAACCTGTCATCTCCA 886
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
|||||
887 GAACCAACCTGTCAAGTATTGAGTGTGAGCCTCATATCAGCACCGATTT 936
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSera 284
|||||
937 GGGGATTCATGAACCTGTACCATCCCTGGCAGCTTCAGCTTACCTGTG 986
284 IacysThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
|||||
987 CATGTACTCTCATCTGCTCACAAGAACTGAGTTAATTGGGAGAAAGAAA 1036
301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG1 317
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1037 ACCATTGTGATCATCTGGAATCTGGTCAAAATCTAGTCCAAATATGTCA 1086
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrAsnProL 334
|||||
1087 AAAATTGGACAAAGTTTCTCAATGATTAAAGAGGTGATTATTAACCCC 1136
334 eupheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
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1137 TCTTCATTTCCAGTGCAGCTATGCTTACTGCTATTTCTGGGTTGGCATTT 1186
351 IleIleTrpLeuAlaArgArgLeuLysGlyLysLysSerLysArgSe 367
|||||
|||||
1187 ATCATTTGCTGGCAAGAGATTAATAAAAAAGGCAAGAAATCCAAAGAGAG 1236
367 rMetAsnAspProTyr 372
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1237 TATGATATGACCATAT 1252
seq_name: /cgn2_6/prodata/2/pna/us6024_COMB.seq:us-60-243-521-8
seq_documentation_block:
; Sequence 8, Application US/60243521
; GENERAL INFORMATION:
; APPLICANT: Hopkins, Christopher M.
; APPLICANT: Peterson, David P.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN ACTIVATED T CELLS
; FILE REFERENCE: PA-0042 P
; CURRENT APPLICATION NUMBER: US/60/243,521
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 2385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Template ID: 331616.2
US-60-243-521-8

alignment_scores:
Quality: 2090.00 Length: 372
Percent Similarity: 99.731 Percent Identity: 98.925
Gaps: 0
alignment_block:
US-09-119-209-2 x US-60-243-521-8
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17 ePheLysLeuTrpGlyTyrPheMetLeuCysCysAspPheLeuAlaHis 34
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187 CTTCAGATTGTGGGGGTGAGCAATGCTGTGTGTGATTTCTGCGCACATC 236
34 IsGlyThrTyrCysTrpThrTyrHisTyrSerGluLysProMetAsnTrp 50
|||||
237 ATGGAACCGACTGCTGACTTACCATTTATTTGAAAAACCAATGAGACTG 286
51 GluArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAlaI1 67
|||||
287 CAAGGGCTAGAAAGATTTCGCCGAGACAAATTACACAGATTAGTTGGCAT 336
67 eglInsnlysaIaGluIleGluThrLeuGluLysThrLeuProPheSera 84
|||||
337 ACMAAACAGGCGGGAATTGAGTATCTGGAGAAAGACACTGCTTCAGTC 386
84 rgseryTyrTrpIleGlyIleArgLysIleGlyIleTrpThrTrp 100
|||||
387 GTTCTTACTACTGATGAGATCCGGAAGATGAGAGAAATATGACCTGCG 436
101 ValGlyThrAsnLysSerLeuThrGluIuAaGluAsnTrpGlyAspG1 117
|||||
437 GTGGGAACCAACAATCTCTTACTGAAAGACGAGAACTGGGGAGATGG 486
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIleL 134
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487 TGAGCCCAACACAGAAAGAAACAAAGAGAGCTGGTGGAATCTATATCA 536

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134 ysArgAsnLysAspAlaGlyLysTrpAsnAspAlaCysHisLysLeu 150
|||||
537 AGAGAAACAAAGATGCGCAAAATGGAAAGATGACGCTGCCCAAAACTA 586
151 LysAlaAlaLeuCysTrpThrAlaSerCysGlnProTrpSerCysSerC 167
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587 AAGGACAGCCCTCTGTTACACACCTTCTTCCAGCCCTGGTCAAGCAGTG 636
167 yHisGlyGlyCysValGluIleLeuAsnAsnHisThrCysAsnCysAsp 184
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637 CCATGAGAAATGTTGTAAGAAATCATCAATATTAACACCTGCACACTGG 686
184 aIGlyTyrTrpGlyProGlnCysGlnLeuValIleGlnCysGlnProLeu 200
|||||
687 TGGGGTACTATGAGGCCCGACAGTGTCACTGTGTGATCATGTGTGAGCTTG 736
201 GAlaIaProGlnLeuGlyThrMetAspCysThrHisProPhedLysnph 217
|||||
737 GAGCCCCCAGACCTGGGTACCATGACCTGTACTACCCCTTTGGGAAACCT 786
217 eSerPheSerSerGlnCysAlaPheSerCysSerGlnGlyThrAsnLeuT 234
|||||
787 CAGCTTCACACTCACAGTGTGCTTCAGCTGCTGTGAAGAAACAACTTAA 836
234 hGlyIleGlnGluThrThrCysGlyProPhedLysnTrpSerSerPro 250
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837 CTGGGATTTGAAGAAACCACTGTGACCATTTGGAAACTGTGCATCTCCA 886
251 GluProThrCysGlnValIleGlnCysGlnProLeuSerAlaProAspLe 267
|||||
887 GAACCAACCTGTCAAGTCAATGAGTGTGAGCCTTATATCAGACACAGATT 936
267 uGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPheThrSerA 284
|||||
937 GGGGATCATGAACCTGAGCATGCCCTGGCCAGCTTCACCTTACTCTTG 986
284 IaCysThrPheIleCysSerGlnGlyThrGluLeuIleGlyLysLys 300
|||||
987 CATGTACCTTCATCTGCTCAGAAAGAACTGATTAATGGGAAAGAA 1036
301 ThrIleCysGlnSerSerGlyIleTrpSerAsnProSerProIleCysG 317
|||||
1037 ACCATTGTGGAATCAATCTGGAATCTGGTCAAACTCAGTCCAAATAGTCA 1086
317 nLysLeuAsnLysSerPheSerMetIleLysGlnGlyAspTyrAsnProL 334
|||||
1087 AAAATTGGCAAAAGTTTCTCAATGATTTAAGAGGGGTGATTATACCCCC 1136
334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
|||||
1137 TCTTCAATTCAGTGGCAGTCATGTTACTGCAATTCCTGGTTGGCATTT 1186
351 IleIleTrpLeuAlaArgArgLeuLysLysGlyLysLysSerLysArgSe 367
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1187 ATCAATTTGGCTGCGCAAGAGATTAAAAAAGCAGAAATCCAAGAGAG 1236
367 rMetAsnAspProTyr 372
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seq\_name: /cgn2\_6/ptodata/2/pna/US093\_COMB.seq:US-09-396-970-8480

seq\_documentation\_block:

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; Sequence 8480, Application US/09396970
; GENERAL INFORMATION:
; APPLICANT: Geating, David P.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A
; TITLE OF INVENTION: MIXED LYMPHOCYTE LIBRARY
; FILE REFERENCE: MLN98-409A
; CURRENT APPLICATION NUMBER: US/09/396,970
; EARLIER FILING DATE: 1999-09-14
; EARLIER APPLICATION NUMBER: 60/100,293

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; EARLIER FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 8756
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 8480
; LENGTH: 2564
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)---(2564)
; OTHER INFORMATION: n = A,T,C or G
US-09-396-970-8480

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alignment_scores:
    Quality: 2090.00      Length: 372
    Ratio: 5.633          Gaps: 0
    Percent Similarity: 99.731    Percent Identity: 98.925

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alignment\_block:

US-09-119-209-2 x US-09-396-970-8480 ..

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17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHis 34
|||||
205 CTTCACAGTTCGTGGGGGTGACACATGCTCTGTGTGATTTCCCTGGCACATC 254
34 IaGlyThrTrpCysTrpThrTrpHisTyrSerGlnLysProMetAsnTrp 50
|||||
255 ATGGAACCGCACTGCTGAGACTTACCATTAATTCGAAAAACCATGAACATG 304
51 GlnArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAlaI 67
|||||
305 CAAGGCGCTAAGAAAGATTCTGCCGAGACATTTACAGATTTAGTTCGCAAT 354
67 eGlnAsnLysAlaGluIleGlyThrLeuGlnLysThrLeuProPheSerA 84
|||||
355 ACAAAACAAAGCGCGGAATTCAGATCTCGAGAAAGACATCTGCCCTTCACATC 404
84 rSerSerTrpTrpIleGlyIleArgLysIleGlyValIleTrpThrTrp 100
|||||
405 GTTCTTACTACTAGATAGGAATCCGGAAAGATAGAGGAATATGAGCTGG 454
101 ValGlyThrAsnLysSerLeuThrGlnGluAlaGluAsnTrpGlyAspC 117
|||||
455 GTGGGACCAACAATCTCTTACTGAAAGACAGAACTGGGGAGATGG 504
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIleL 134
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505 TCAGGCCCAACAACAAGAAAGACAGAGCATGCGGAGATCTATATCA 554
134 ysArgAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
|||||
555 AGAGAAACAAAGATGCGCAAAATGGAAAGATGACGCTGCCCAAAACTTA 604
151 LysAlaAlaLeuCysTrpThrAlaSerCysGlnProTrpSerCysSerC 167
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605 AAGGACAGCCCTCTGTTACACAGCTTCTTCCAGCCCTGGTCAATGCAAGTG 654
167 yHisGlyGlyCysValGluIleLeuAsnAsnHisThrCysAsnCysAsp 184
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655 CCATGAGAAATGTTGTAAGAAATCATCAATATTAACACCTGCACACTGGAGTG 704
184 aIGlyTyrTrpGlyProGlnCysGlnLeuValIleGlnCysGlnProLeu 200
|||||
705 TGGGGTACTATGAGGCCCGACAGTGTGTGATTTGATGTGAGCCTTTTG 754
201 GAlaIaProGlnLeuGlyThrMetAspCysThrHisProPhedLysnph 217

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|||||
755 GAGGCCCGAGCTGGTACCATGACGTGACTACCCCTTGGGAAACTT 804
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuT 234
805 CAGCTTCAGCTCAGAGTGTGCTTACGCTCTGTAAGGAACAACCTTAA 854
234 hGlyYlIeGluGluThrThrCysGlyPropheGlyAsnTrpSerSerPro 250
855 CTGGGATTGGAAGAAACCACTGTGTGACCATTTGGAACTGTCATCTCCA 904
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
905 GAACCAACCTCTCAAGTATTCAGTGTAGCCCTCTATCAGCACCAATTT 954
267 uGlyYlIeMetAsnCysSerHisProLeuAlaSerPheSerPheThrSera 284
955 GGGGATCATGAACTGTAGCCATCCCTGGCCAGCTTACGCTTTACCTCTG 1004
284 lAcYThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLys 300
1005 CATGTACCTTCATCTGCTCAGAAAGAACTGAGTTAATTGGGAAGAA 1054
301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG 317
1055 ACCATTGTGATCATCTGGAATCTGTCAAATCCTAGTCCAAATATGTCA 1104
317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTrpAsnProL 334
1105 AAATTGTGCAAAAGTTTCTCAATGATTAAGAGGATGATTTAACCCCC 1154
334 eupheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
1155 TCTTCATCCAGTGGCAGTCATGTTACTGTCATCTCTGGTTGGCATTT 1204
351 lIleIleTrpLeuAlaArgArgLeuLysLysGlyLysSerLysArgSe 367
1205 ATCATTTGGTGGCAAGAGATTAAAAAAGCAAGAAATCCAAAGGAAG 1254
367 rMetAsnAspProTyr 372
1255 TATGAATGACCCCATAT 1270

seq_name: /cgn2_6/plodata/2/pna/US6017_COMB.seq:us-60-172-373-15742

seq_documentation_block:
; Sequence 15742, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: Method for the identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0006_P
; CURRENT APPLICATION NUMBER: US/60/172,373
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 15742
; LENGTH: 2387
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 331616.2
US-60-172-373-15742

alignment_scores:
Quality: 2082.00 Length: 372
Ratio: 5.627 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.656

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alignment_block:
US-09-119-209-2 x US-60-172-373-15742
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17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHis 34
189 CTTCAAGTTGGGGGTGGACATGCTCTGTTGATTTCTGCGCACATC 238
34 lGlyYlIeThrCysTrpThrTrpHisIleSerGluLysProMetAsnTrp 50
239 ATGGAACCCAGCTGTGACTTACCATTTATCTGAAAAAACCATGAACTGG 268
51 GlnArgAlaArgArgPheCysArgAspAsnTrpThrAspLeuValAlaI 67
289 CAAAGGCTAGAGATTTCTGCCGAGACAAATTACACAGATTAGTTGCCAT 338
67 eGlnAsnLysAlaGluIleGluTrpLeuGluLysThrLeuProPheSera 84
339 ACAAAACAAGCGGAAATTGATATCTGGAGAAAGACTCTGCTTACATC 388
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: Sequence 292, Application US/60118318
: GENERAL INFORMATION:
: APPLICANT: Roopa, Reddy
: APPLICANT: Guejler, Karl, J.
: APPLICANT: Au-Young, Janice
: TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
: FILE REFERENCE: PA-0013 P
: CURRENT APPLICATION NUMBER: US/60/118,318
: CURRENT FILING DATE: 1999-02-01
: NUMBER OF SEQ ID NOS: 306
: SOFTWARE: PERL Program
: SEQ ID NO 292
: LENGTH: 2385
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: -
: OTHER INFORMATION: 1876370CB1
US-60-118-318-292
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Ratio: 5.604          Gaps: 0
Percent Similarity: 99.731      Percent Identity: 98.118
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; Sequence 1, Application PC/TUS9203970
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc.
; TITLE OF INVENTION: LEUKOCYTE-ASSOCIATED CELL SURFACE
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/03970
; FILING DATE: 19920513
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Heine, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DECI-152Bq9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; TELEX: 940675
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2330 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 53..1210
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
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TELECOMMUNICATION INFORMATION:

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: Sequence 1, Application US/08340539
: GENERAL INFORMATION:
: APPLICANT: Tedder, Thomas F.
: APPLICANT: Kansas, Geoffrey S.
: TITLE OF INVENTION: CHIMERIC SELECTINS AS SIMULTANEOUS
: TITLE OF INVENTION: BLOCKING AGENTS FOR COMPONENT SELECTIN FUNCTION
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
: STREET: Ten Post Office Square
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/340,539
: FILING DATE: 16-NOV-1994
: CLASSIFICATION: 514

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/008,459
: FILING DATE: 25-JAN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/983,606
: FILING DATE: 30-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/862,483
: FILING DATE: 02-APR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/770,608
: FILING DATE: 03-OCT-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/737,092
: FILING DATE: 29-JUL-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/730,503
: FILING DATE: 08-JUL-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/700,773
: FILING DATE: 15-MAY-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/313,109
: FILING DATE: 21-FEB-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Heine, Holliday C.
: REGISTRATION NUMBER: 34,346
: REFERENCE/DOCKET NUMBER: DECI-318XX
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-2290
: TELEFAX: (617) 451-0313
: FAX: 940675
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2330 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 53..1210
: PUBLICATION INFORMATION:
: DOCUMENT NUMBER: US 07/700,773
: FILING DATE: 15-MAY-1991
: US-08-340-539-1

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Quality: 2076.00 Length: 372
Ratio: 5.611 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.118

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seq.documentatation_block:
; Sequence 1, Application US/08410569
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; APPLICANT: Sperlini, Olivier G.
; TITLE OF INVENTION: LEUCOCYTE ADHESION MOLECULE-1 (LAW-1)
; TITLE OF INVENTION: AND LIGAND THEREOF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
; STREET: Ten Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,569
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,608
; FILING DATE: 03-OCT-1991
; APPLICATION NUMBER: US 07/700,773
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Helme, Holliday C.
; REGISTRATION NUMBER: 34,346
; REFERENCE/DOCKET NUMBER: DCG-152EX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-2290
; TELEFAX: (617) 451-0313
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
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; US-08-410-569-1

alignment_scores:
Quality: 2076.00 Length: 372
Ratio: 5.611 Gaps: 0
Percent Similarity: 99.462 Percent Identity: 98.118

alignment_block:
US-09-119-209-2 x US-08-410-569-1 ..

Align seg 1/1 to: US-08-410-569-1 from: 1 to: 2330

1 MetIlePheProTIPtPysCysGlnSerThrGlnArgAspLeuTPaSnI 17
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92 ATGATATTTTCATGGAATATGTCAGAGACCGCAGAGGAGACTTATGGAATAT 141

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17 ePhelYsLeuTrpGlyTrpThrMetLeuCySCysAspPheLeuAlaHisH 34
142 CTTCAAGTTGTGGGGTGACAAATGCTGTTGTGATTTCCTGGGCATC 191
34 IAGLYThrTyrCysTrpThrTyrHisIstYrSerGluYsPromeLsnTrp 50
192 ATGGAAACGACAGTGGAGATTACATTTATCTGAAAACCCATGAACTGG 241
51 GlnATGAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAlaI 67
242 CAAAGGGCTAGAGATTTCTGGCGAGACATTAACAGATTAGTGGCCAT 291
67 eGlnAsnLysAlaGluIleGluTyrLeuGluYsThrLeuProPheSerA 84
292 ACAAAACAAGCGGGAATTTGAGTATCTGGAGAAAGACTGCGCTTTCAGT 341
84 rGSeTyrTyrTrpIleGlyIleArgLysIleGlyIleTrpThrTrp 100
342 GTTCTTACTAGTGGATAGGAATCCGGAAGATAGGAGAAATATGACGTGG 391
101 ValIGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAspG 117
392 GTGGGAACCAACAATCTCTCACTGAAGAGCAGAACTGGGGAGATGG 441
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTyrIleL 134
442 TCAGCCCAACAACAAGAAACAAGAGAGACTGCGTGGAGATCTATATCA 491
134 ySarGAsnLysAspAlaGlyLysTrpAsnAspAspAlaCysHisLysLeu 150
492 AGAGAAACAAGATGACAGCAATGGAACGATGACGCTGCACAAACTA 541
151 LysAlaIalaLeuCystrTyrThrAlaSerCysGlnProTrpSerCysSer 167
542 AAGGAGCCCTCTGTACACAGCTTCTTGGCAGCCCTGGTCAATGACGTGG 591
167 yHisGlyGluCysValGluIleIleAsnAsnHisThrCysAsnCysAspY 184
592 CCATGGAGAAATGTCAGAAATCATCAATTAATACACCTGCACACTGGATG 641
184 aGlyTyrTyrGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
642 TGGGCTACTATGGGCCCACTGCTCAGTTGTGATTCAGTGTAGCCCTTGG 691
201 GluAlaProGluLeuGlyThrMetAspCysThrHisProPheGlyAsnH 217
692 GAGGCCCAAGACTGGGTACCATGACTGTACTCAACCCTTGGGAAACTT 741
217 eSerPheSerSerGlnCysAlaPheSerCysSerGluGlyThrAsnLeuT 234
742 CAACCTTCAACTCACAGTGTGCTTCACTGCTCTGAAGAGACAAACTTAA 791
234 hGlyIleGluGluThrThrCysGlyProPheGlyAsnTrpSerSerPro 250
792 CTGGGATTGGAAGAAACAACCTGTGAACCATTTGGAACCTGGTCACTCCA 841
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
842 GAACCAACCTGTCAAGTATTCAGTGTGAGCTCTATCAGCACCAAGATT 891
267 uGlyIleMetLsnCysSerHisProLeuAlaSerPheSerPheThrSerA 284
892 GGGGATCATGAACCTTACCATCCCTGGCCAGCTTTCAGCTTATACCTCTG 941
284 IaCysThrPheIleCysSerGluGlyThrGluLeuIleGlyLysLysLys 300
942 CATGATACCTTCATCTGCTCAGAAAGAACTGAGTTAATTGGGAAGAA 991
301 ThrIleCysGluSerSerGlyIleTrpSerAsnProSerProIleCysG 317
992 ACCATTGTGAAATCATCTGGAATCTGGTCAAAATCTAGTCCAAATATGTCA 1041

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317 nLysLeuAspLysSerPheSerMetIleLysGluGlyAspTyrAsnProL 334
1042 AAAATTGGACAAAGTTTCTCAATGATTAAGGAGGTGATTATAACCCCC 1091
334 euPheIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
1092 TCTTCACTTCAGTGGCAGTCATGTTACTGTCATTTCTGTGGTTGGCATTT 1141
351 IleIleTrpLeuAlaArgArgLeuLysLysGlyLysSerLysArgSe 367
1142 ATCATTTTGGCTGGCAAGAGATTAAAAAAGCCAGAAATCCACAGAGAG 1191
367 rMetAsnAspProTyr 372
1192 TATGAATGACCCCATAT 1207

seq_name: /cgn2_6/p/ctdata/2/pna/US6021_COMB.seq:US-60-212-659-816

seq_documentation_block:
: Sequence 816, Application us/60212659
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
: FILE REFERENCE: CLO00674
: CURRENT APPLICATION NUMBER: US/60/212, 659
: NUMBER OF SEQ ID NOS: 879
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 816
: LENGTH: 3238
: TYPE: DNA
: ORGANISM: HUMAN
US-60-212-659-816

alignment_scores:
Quality: 1883.00 Length: 345
Ratio: 5.538 Gaps: 0
Percent Similarity: 98.551 Percent Identity: 97.391

alignment_block:
US-09-119-209-2 x US-60-212-659-816 ..

Align seg 1/1 to: US-60-212-659-816 from: 1 to: 3238

22 GIYTrpThrMetLeuCySCysAspPheLeuAlaHisHISGLYThrTyrCy 38
1811 GGATATTTTCTTCCAAAGCAAGATTTCTGGCAGCATCATGAAACCGACTG 1860
38 sTrpThrTyrHisTyrSerGluYsPromeLsnTrpGlnArgAlaArgA 55
1861 CTGGACTTACCATTTATTTCTGAAAAACCCATGAATGAGCAAGGGCTAGA 1910
55 rGPhCysArgAspAsnTyrThrAspLeuValAlaIleLsnLysAla 71
1911 GATTCGCCGAGACAATTACACAGATTTAAGTTCATACAAAAACAAGCGG 1960
72 GluIleGluTyrLeuGluYsThrLeuProPheSerArgSerTyrTyrTr 88
1961 GAAATTGAGTATCTGAGAGAACTGCTGCTTCACTGCTTACTACTAGC 2010
2011 GATAGGAATCCCGAAGATAGGAGAAATATGACGCTGGGGGAGAACCAACA 2060
105 ySerLeuThrGluGluAlaGluAsnTrpGlyAspGlyGluProAsn 121
2061 AATCTCTTACTGAGAGACGAGAACTGCGGAGATGTACCCCAACAAAC 2110
122 LysLysAsnLysGluAspCysValGluIleTyrIleLysArgAsnLysAs 138

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2111 AAGAGAACAGAGAGACTGCTGGAGATCTATATCAAGAGAACCAAGA 2160
138 palaglylytTpasnaspaspalaCyhislysluysalalaLauC 155
1261 TCGAGGCAAAATGAGACGATGAGCCCTGGCACAACTAAAGCAGCCCTCT 2210
155 ySTy-ThrAlaSerCySGInProTTPSerCySerglyHislygluCyS 171
2211 GTTACACAGACTCTTGGCCAGCCCTGGTCATGACGAGCCATGAGAAATGT 2260
172 ValgluileleasnasnHisThrCysasnCySaspValglytyrtygl 188
2261 GTAGAAATCAATCAATTAATACCTGCAACTGTATGTGGGGTACTATGG 2310
188 yProGInCySGInleuValIlegInCySGluProleuGluAlaProGluL 205
2311 GCCCCAGCTGAGCTTGTGATTCAGTGTGAGCCCTTGGAGGCCCCAGAGC 2360
205 euGlyThrMetAspCySthrHisProPhelGlyAsnPheserPheSer 221
2361 TGGGTACCATGACTGTACTCTACCCCTTGGGAAACTTTCACCTTCAGCTCA 2410
222 GInCySAlaPheSerCySergluGlyThrAsnleuthrGlyIleglu 238
2411 CAGTGTGCTCAGCTGCTCTGAAGAGAACTTACTGAGATGAGAGA 2460
238 uThrThrCySGlyProPhelGlyAsnTPSerSerProGluProThrCySg 255
2461 AACCACTGTGGACCATTTGGAACCTGTGCATCTCCAGAACCAACCTGTC 2510
255 InValIlegInCySGluProleuSerAlaProAspleuGlyIleMetAs 271
2511 AAGGATTCAGTGTGAGCCCTTATCAGACCAATTTGGGGATCAATGAAAC 2560
272 CySserHisProleuAlaSerPheSerPheThrSerAlaCySThrPheI 288
2561 TGTAGCCATCCCTGGCCAGCTTACCTTACCTGATGACTTCAAT 2610
288 eCySserGluGlyThrGluLeuIlegIlysluyslyThrIlegysglus 305
2611 CTGCTCAGAAAGAACTGAGTTAATTTGGGAGAGAAACCATTTGTGAAT 2660
305 eISerGlyIleTPSerAsnProSerProIleCySGInlysluysAsplys 321
2661 CATCTGGAATCTGTGTCAAATCTAGTCCAAATATGTCAAAATTTGGACAAA 2710
322 SerPheSerMetIleysgluGlyAspTyraSnProleuPheIleProVa 338
2711 AGTTTCTCAATGATTAGAGAGGATGATTATAACCCCTTCTCATTCAGAT 2760
338 lAlaValMetValThrAlaPheSerGlyLeuAlaPheIleIleTPLeua 355
2761 GCAGAGTCAGTGTACTGATCTCTGGGTTGGCATTTATCATTTGGCTGG 2810
355 lAArgArGleuLyslysglylysluysSerlySarg 366
2811 CAAGGAGATTAAAAAAGGCAAGAAATCCAGACAGA 2845
seq_name: /cgn2_6/ptodata/2/pna/us091_COMB.seq:us-09-119-209-3
seq_documentation_block:
; Sequence 3, Application US/09119209
; GENERAL INFORMATION:
; APPLICANT: LASKY, LAURENCE A.
; APPLICANT: STACHELL, SCOTT E.
; APPLICANT: ROSEN, STEVEN D.
; APPLICANT: SINGER, MARK S.
; APPLICANT: YEDNICK, TED A.
; TITLE OF INVENTION: LYMPHOCYTE HOMING RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way

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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/119,209
; FILING DATE: 20-Jul-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/513278
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/059027
; FILING DATE: 6-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/786149
; FILING DATE: 31-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/315015
; FILING DATE: 23-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0565D1C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2214 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-09-119-209-3

alignment_scores:
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Ratio: 4.988 Gaps: 0
Percent Similarity: 88.978 Percent Identity: 76.075

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US-09-119-209-2 x US-09-119-209-3 ..
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106 ATGCTGTTTCCATGAGATGTGAGGTACTTACTGGGGCTCGAGGAGACAT 155
17 ePheLysLeuTPGlyTYrPThrMetLeuCySAspPheLeuAlaHis 34
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
156 CTTGAAGCTGTGGCTGTGACACTGCTCTGTTGTGACTTCCGATACACC 205
34 IsGlyThrTyCySTrpThrTyTrHisTySerGluLysProMetAsnTrp 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
206 ATGGAATCTACGTGTGGACTTACCATTTATCTGAAAACCCCATGAACTGG 255
51 GlnArgAlaArgArgPheCySArgAspAsnTyTrpAspLeuValAlaIle 67
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
256 GAAATGCTAGAAAGTTCTGCAGCAAAATTCACACAGATTAGTGGCCAT 305
67 eGlnAsnLysAlaGluIlegLyuTyrlLeuGluLysThrLeuProPheSerA 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
306 ACAAAACAGAGAGAAATTTAGATATTAGAGAAATACATTGGCCCAAAAGCC 355
84 rGSerTyTrpTrpIlegIlyleArgLysIleglyGlyIleTPThrTrp 100
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356 CTTATTTACTACTGCATVAGGAATCAGAGAAATTTGGCAAAATGTGGACATGG 405
101 ValGlyThrAsnLysSerLeuThrGluGluAlaGluAsnTrpGlyAspG1 117
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
406 GTGGAGAACCAACAACATCTCTACATTAAGACAGACAGAACTGGGGTCTGG 455
117 yGluProAsnAsnLysLysAsnLysGluAspCysValGluIleTrpIle1 134
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
456 GGAGACCAACAACAAAGAGTCCAAAGGAGGAGACTGTGTGGAGATCTAATAC 505
134 ysArGAsnLysAspAlaGlyLysTrpAsnAspAlaIleCysHisLysLeu 150
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
506 AGAGGGAGACGAGACTCTGGGAAATGGAAACGATGAGAGCCGTGCACAAACA 555
151 LysAlaIleLeuCysTrpTrpAlaSerCysGlnProTrpSerCysSerG1 167
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
556 AAGCGACACTCTCTCTACACAGCCCTTTGGCCAGCCAGGCTCTTGCATGG 605
167 yHisGlyLysCysValGluIleIleAsnAsnHisThrCysAsnCysAspY 184
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
606 CCGTGAGAAATGTGTGAAACATCAACATCAACATCACAGTCACTGTGGATG 655
184 aLgLyTrpTrpGlyProGlnCysGlnLeuValIleGlnCysGluProLeu 200
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
656 CAGGGTTTACGGGCCCCAGTGTCTGATGTGGTCCAGTGTAGGCTTTGG 705
201 GluAlaProGluLeuGlyThrMetAspCysTrpHisLysProGheGlyAsnPh 217
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
706 GAGGCCCTCAGTTGGGTACCATGGACATGCATCCACCCCTTGGAAACTTT 755
217 eSerPheSerSerGlnCysAlaPheSerCysSerGlnGlyThrAsnLeuT 234
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
756 CACGTTTCAGTCCAAAGTGTCTTTCACATGTTCTGAGGGAAGACACTAC 805
234 hrgLylIleGluGluThrThrCysGlyProPheGlyAsnTrpSerSerPro 250
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
806 TTGGGAGTCGAGAAACACAGTGTGGAGCATCTGGAAACGTGCATCTCCA 855
251 GluProThrCysGlnValIleGlnCysGluProLeuSerAlaProAspLe 267
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
856 GAGCCATCTTCGCCAAGTGTCTCAGCTGTACGCTTTGGAGGCCCTTGAGTT 905
267 uGlyIleMetAsnCysSerHisLysProLeuAlaSerPheSerPheThrSera 284
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
906 GGGTACCATGGACATGCATCCACCCCTTGGAAACTTCACGTTCCAGTCCA 955
284 IeCysThrPheIleCysSerGluGlyTrpGluLeuIleGlyLysLysLys 300
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
956 AGGTGTCTTTCACACTGTTCTGAGGGAAGAGCTACTTGGGAGTCGACGANA 1005
301 ThrIleCysGlnSerSerGlyIleTrpSerAsnProSerProIleCysG1 317
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
1006 ACACAGTGTGGAGCATCTGCAGAACTGGTCACTCTCCAGAGCCCAATCTGCCA 1055
317 nLysLeuAspLysSerPheSerMetIleLysGluGluLysPTrAsnProL 334
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
1056 ACAGACAAACAGAGATTCTCAAGATGACAAAGAGAGAGTGTACCAACCCCC 1105
334 eupHeIleProValAlaValMetValThrAlaPheSerGlyLeuAlaPhe 350
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
1106 TCTTCAATCTCTGTAGCCGTATGTGTACCCGCAATCTCTGGGGCTGGCATTT 1155
351 IleIleThrPheLeuAlaArgArgLeuLysGlyLysLysSerLysArgSe 367
||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
1156 CTCATTTGGCTGGCAAGCGCTTAAAAAAGGCAGCAGAATCTCAAGAAAG 1205
367 rMetAsnAspProTrpY 372
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1206 GATGGATGATGCATAC 1221
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seq_documentation_block:

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; Sequence 2748, Application US/60230435
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLO00768
; CURRENT APPLICATION NUMBER: US/60/230,435
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 2991
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2748
; LENGTH: 3238
; TYPE: DNA
; ORGANISM: HUMAN
US-60-230-435-2748

alignment_scores:
      Quality: 1304.00      Length: 330
      Ratio: 4.657      Gaps: 6
Percent Similarity: 84.848      Percent Identity: 77.273

alignment_block:
US-09-119-209-2 x US-60-230-435-2748 ..

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1815 TCCTTTTCTACTCTCCCAACCATGMACTGGCAAGGGCTGAMGATT 1864

56 ecysatcaspasntyrthrapsleuValAlaIleGlnAsnLysAlaLui 73
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1865 CTCGCCAGACAATTACACAGATTAGTTGCCATACAAACACAGCGGAAA 1914

73 leGIuTrLeuGluLysThrLeuProPheSerArgSerTyrTyrPile 89
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1915 TTGAGTATCTCGAAGAAGACTCGCCTTTCAGTGGCTTCTTACTGTGATA 1964

90 GlyTlleArgLysTlleGlyGlyIleTrpThrTrpValGlyThrAsnLysS 106
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1965 GGAATCCGGAGATAGAGGAATATGACGCTGGTGGAAACCAACAAATC 2014

106 rIeuTrHGIuAlaGluAsnTrpGlyAspGlyLupProAsnAsnLysL 123
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2015 TCTTTACTGAAGAAGCACAGAACTGGGAGATGGTACCCCAACACACAGA 2064

123 ysAsnLysGluAspCysValGluIleTyrIleLysAlaGAsnLysAspAla 139
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2065 AGAACAAAGAGGAGCTGGGTGAGATCTATATCAAGACAAACAAAGATGCA 2114

140 GlyLysTrpAsnAspAspAlaCysHisLysLeuLysAlaAlaLeuCysTy 156
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2115 GGCMAATGGAACGATGACGCCCTGCCAACMAACTAAAGCACCCCTGTGA 2164

156 rTrpAlaSer.....CysGlnProTrpSerCysSerGlnHisGlyLus 171
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2165 CACAGGAGGAGCTGACAAAGCGGTATAGCTGGCTCAGACTCAGAAAGGG 2214

171 ysValGluIleIleAsnAsnHisThrCysAsnCysAspValGlyTyrTr 187
   :::::  ||||| ||||| ||||| ||||| ||||| ||||| |||||
2215 CCAACG.....ATCAATTAATTACACCTGCACAACGTGATGTGGGTACTAT 2258

188 GlyProGlnCysGln.....LeuValIleGlnCysGluProLe 200
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2259 GGGCCCCAGGTGCTGTTGGTAACTCTTTCCTTCTTGGCTTCTTCTT 2308

200 uGIuAlaProGluLeuGlyThrMetAspCysTrpHisProPhGlyAsn 217
   |.....:::  ||||| ||||| ||||| ||||| ||||| |||||
2309 AGGTAA.....GTCACAGGAATCACTCACCCCTTTGGGAACACT 2346

217 heserPheSerSerGlnCysAlaPheSerCysSerGluGlyTrnAsnLeu 233

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```
|||||
2347 TCAGCTTAGCTCACAGTGTGCTTCACTCTGAGGAAACAACCTA 2396
2348 ThrGlyIleGluGluThrThrCysGlyProPheGlyAsnTrpSerSerPr 250
2397 ACTGGGATTGAAGAAACCACCTGTGACCATTTGAAACAGTGTCTCTCC 2446
250 OgluProThrCysGluVal.....IleGluCysGluProLeuSerAlap 265
|||||
2447 AGAACCAACCTGTCAGGTGAGTAACCTCAGACTAGAGGTTTGTCTATGC 2496
265 roAspLeuGlyIleMetAsnCysSerHisProLeuAlaSerPheSerPhe 281
2497 AATACCTGGGCTTACAG.....AGCCATCCCTGGCCAGCTTCAGCTTT 2540
282 ThrSerAlaCysThrPheIleCysSerGluGlyThrGluLeuIleGlyLy 298
2541 ACCTGTGATGTACCTCATCTGCTCAGAAAGAACTGATTATGTGGAA 2590
298 slyGlyThrIleCysGluSerSerGlyIleTrpSerAsnProSerProI 315
2591 GAAGAAACCATTTGTGAATCATCTGGAATCTGTCAATCTCAAGTCCAA 2640
315 IecysGluIlySleuAspIlySerPheSerMetIleIlySgluGlyAspTyr 331
|||||
2641 TATGTCAAAGTGAGTAAGTTGTCTCTGGAAACTGAAATCTTAACGATGG 2690
332 AsnProLeuPheIleProValAlaValMetValThrAlaPheSerGlyLe 348
2691 AGCTGATGTGTTTCATTCACGTGCGCATGTGTTACTGCAATCTCTGTGGTT 2740
348 uAlaPheIleIleTrpLeuAlaArgArgLeuIlySgly 361
|||||
2741 GGCATTTATCATTTGGCTGCGCAGAGATTAAAAAAGGT 2780
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2001, 21:40:24 ; Search time 70.99 seconds

(without alignments)  
355.811 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MIFPWKOSTORDLNFKL.....WLARRLKGGKSKSRMNDPY 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

#### SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	2090	98.8	385	1 A34015	L-selectin precurs
2	1992	94.1	372	2 JC5377	L-selectin precurs
3	1796	84.9	376	2 JC4892	L-selectin precurs
4	1682	79.5	370	2 S22124	L-selectin precurs
5	1653	78.1	372	2 S23936	L-selectin precurs
6	1652	78.1	372	1 S09702	L-selectin precurs
7	1651	78.0	372	1 A32375	L-selectin precurs
8	905	42.7	830	2 A30359	P-selectin precurs
9	902.5	42.7	768	2 A42755	P-selectin precurs
10	894.5	42.3	646	2 JN0473	P-selectin precurs
11	885	40.7	768	2 I53821	P-selectin - rat
12	862	40.7	610	2 A35046	E-selectin precurs
13	861	40.5	551	2 I46709	endothelial leukoc
14	857	40.5	612	2 S23174	endothelial leukoc
15	857	40.5	618	2 B42755	E-selectin precurs
16	849.5	40.1	485	2 S36772	E-selectin - bovin
17	815.5	38.5	482	2 JC5092	E-selectin - pig
18	236	11.2	868	2 T20239	hypothetical prote
19	212.5	10.0	473	2 B38738	coagulation factor
20	212.5	10.0	1019	2 A38738	coagulation factor
21	199.5	9.4	449	1 NBH0HS	complement factor
22	199.5	9.4	1231	1 NBH0HS	complement factor
23	175.5	8.3	2014	2 I36936	complement recepto
24	172	8.1	2489	2 I73012	complement C3b/C4b
25	171.5	8.1	597	1 S53711	C4BP alpha chain p
26	170	8.0	404	2 A46274	HIV gp120-binding
27	168	7.9	2132	1 A55182	aggreccan precursor
28	167	7.9	321	1 LNH0ER	IgE Fc receptor II
29	167	7.9	1234	1 NBMSH	complement factor

30	166.5	7.9	558	2 S57953	C4BP protein alpha
31	166	7.8	1456	1 A36563	mannose receptor p
32	165.5	7.8	1560	2 T16833	hypothetical prote
33	165.5	7.8	1479	2 T42710	mannose receptor,
34	165	7.8	311	1 LNH02A	asialoglycoprotein
35	164.5	7.8	482	2 A34924	complement C3b/C4b
36	163	7.7	669	2 S65551	factor II - bovine
37	163	7.7	2124	2 A28452	proteoglycan core
38	162.5	7.7	345	1 NBBO	apolipoprotein H p
39	162	7.7	304	2 JX0209	lectin, galactose/
40	162	7.7	600	2 S62786	aggreccan - human
41	162	7.7	1574	2 T13954	MEGF6 protein - ra
42	161	7.6	469	1 NBMSC4	C4b-binding protei
43	160.5	7.6	1455	1 A48925	mannose receptor p
44	160	7.6	638	2 S08042	proteoglycan core
45	160	7.6	1091	1 PL0009	complement C3d/Eps

#### ALIGNMENTS

RESULT 1  
A34015  
L-selectin precursor, long splice form - human  
N:Alternate names: CD62L; leucocyte cell adhesion molecule-1 (LECAM-1, LAM-1); leukoc  
ral lymph node homing receptor Leu-8  
C:Species: Homo sapiens (man)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
C:Accession: I55333; S06798; JLO104; A34015; A33912  
R:Ord, D.C.; Ernst, T.J.; Zhou, L.J.; Rambaldi, A.; Spertini, O.; Griffin, J.; Tedder  
J. Biol. Chem. 265, 7760-7767, 1990  
A:Title: Structure of the gene encoding the human leukocyte adhesion molecule-1 (TQ1,  
A:Reference number: I55333; MUID:90243637  
A:Accession: I55333  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 14-385 <ORD>  
A:Cross-references: GB:M32414; NID:q187259; PIDN:AA60700.1; PID:g386860  
R:Cametini, D.; James, S.P.; Stamenkovic, I.; Seed, B.  
Nature 342, 78-82, 1989  
A:Title: Leu-8/TQ1 is the human equivalent of the Mel-14 lymph node homing receptor.  
A:Reference number: S06798; MUID:90044046  
A:Accession: S06798  
A:Molecule type: mRNA  
A:Residues: 1-225, 'S', 227-385 <CAM>  
A:Cross-references: EMBL:X17519; NID:q34344; PIDN:CA843536.1; PID:g4902829  
A:Note: this translation is not annotated in GenBank entry HSL808, release 111.0  
R:Redder, T.F.; Isaacs, C.M.; Ernst, T.J.; Demetri, G.D.; Adler, D.A.; Distche, C.M.  
J. Exp. Med. 170, 123-133, 1989  
A:Title: Isolation and chromosomal localization of cDNAs encoding a novel human lymph  
oetins.  
A:Reference number: JLO104; MUID:89310350  
A:Accession: JLO104  
A:Molecule type: mRNA  
A:Residues: 1-230, 'N', 232, 'N', 234-254, 'E', 256-385 <TED>  
A:Cross-references: GB:X16150; NID:q34428; PIDN:CAA34275.1; PID:g34429  
A:Note: the translated sequence in GenBank entry HSLVMI, release 111.0, differs from  
R:Bowen, B.R.; Nguyen, T.; Laskey, L.A.  
J. Cell Biol. 109, 421-427, 1989  
A:Title: Characterization of a human homologue of the murine peripheral lymph node ho  
A:Reference number: A34015; MUID:89308881  
A:Accession: A34015  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 14-49, 'Y', 51-190, 'H', 192-205, 'L', 207-226, 'F', 228-385 <BOW>  
A:Cross-references: GB:X16070; NID:g38092; PIDN:CAA34203.1; PID:g38093  
R:Siegelman, M.H.; Weisman, I.L.  
Proc. Natl. Acad. Sci. U.S.A. 86, 5562-5566, 1989  
A:Title: Human homologue of mouse lymph node homing receptor: evolutionary conservati  
A:Reference number: A33912; MUID:89315837  
A:Accession: A33912  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 14-205, 'L', 207-385 <SITE>  
A:Cross-references: GB:M25280; NID:9187182; PIDN:AAC63053.1; PID:9307134  
C:Comment: For an alternative splice form, see PIR:S09702.  
C:Genetics:  
A:Gene: GDB:SELL; GDB:LNHR; LSEL; LAM1; LYAM1; LAM-1  
A:Cross-references: GDB:120157; GDB:118834; OMIM:153240  
A:Map position: 1q22-1q23  
A:Introns: 14/3; 42/1; 171/1; 207/1; 269/1; 331/1; 374/1; 380/2  
C:Function:  
A:Description: binds with low affinity to oligosaccharides like heparan sulfate and sialyl  
ment of leucocytes to areas of inflammation, and with CD162 mediates neutrophil-neutroph  
C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology;  
C:Keywords: alternative splicing; cell adhesion; duplication; glycoprotein; inflammation  
F:1-51/Domain: signal sequence #status predicted <SIG>  
F:42-168/Domain: C-type lectin homology <LCH>  
F:52-385/Product: L-selectin #status predicted <MNT>  
F:52-343/Domain: extracellular #status predicted <EXT>  
F:173-204/Domain: EGF homology <EGF>  
F:210-267/Domain: complement factor H repeat homology <FHL>  
F:272-329/Domain: complement factor H repeat homology <FHL>  
F:344-368/Domain: transmembrane #status predicted <TM>  
F:369-385/Domain: intracellular #status predicted <INT>  
F:73,117,190,245,259/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:377,380/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 98.8%; Score 2090; DB 1; Length 385;  
Best Local Similarity 98.9%; Pred. No. 5,6e-148;  
Matches 368; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MIFPMKOSTORDLNMIFKLMGWTMLCCDFLAHHGTCWTHYSEKPMNMOARRECRDN 60  
|||||  
DB 14 MIFPMKOSTORDLNMIFKLMGWTMLCCDFLAHHGTCWTHYSEKPMNMOARRECRDN 73  
|||||

QY 61 YTDLVAIONKAEIYELEKTLPEFSRSYWIIGIRKIGITWVGINKSLTEAEENMGDGEPN 120  
|||||  
DB 74 YTDLVAIONKAEIYELEKTLPEFSRSYWIIGIRKIGITWVGINKSLTEAEENMGDGEPN 133  
|||||

QY 121 NKKNKEDCEVEIYIKRNKADAGKNDACHKRLKALCYTASCPWSCSGHGECEVEIINNHTC 180  
|||||  
DB 134 NKKNKEDCEVEIYIKRNKADAGKNDACHKRLKALCYTASCPWSCSGHGECEVEIINNHTC 193  
|||||

QY 181 NCDVGYGPOQOLVIOCEPLEAPELGTMCTHPFGNFSFSQCAFSCSEGNLTGIEETT 240  
|||||  
DB 194 NCDVGYGPOQOLVIOCEPLEAPELGTMCTHPFGNFSFSQCAFSCSEGNLTGIEETT 253  
|||||

QY 241 CGPFGNMSSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTSACTFCSEGTTELIGKK 300  
|||||  
DB 254 CGPFGNMSSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTSACTFCSEGTTELIGKK 313  
|||||

QY 301 TICSSGIMSNPSPICQKLDKSFMSIKEGDYNPFLTIPVAVMTAFSGLAFTIIMLARLKK 360  
|||||  
DB 314 TICSSGIMSNPSPICQKLDKSFMSIKEGDYNPFLTIPVAVMTAFSGLAFTIIMLARLKK 373  
|||||

QY 361 GKSKRSMDPY 372  
|||||  
DB 374 GKSKRSMDPY 385  
|||||

RESULT 2  
JC5377  
L-selectin precursor - hamadryas baboon  
C:Species: Papio hamadryas (hamadryas baboon)  
C:Date: 02-Jun-1997 #sequence\_revision 12-Sep-1997 #text\_change 21-Jan-2000  
C:Accession: JC5377; PC4315  
R:Tsunashita, N.; Fu, H.; Berg, E.L.  
A:Title: PCR cloning of the cDNA encoding baboon L-selectin.  
A:Reference number: JC5377; MUID:97128794  
A:Accession: JC5377  
A:Molecule type: mRNA  
A:Residues: 1-372 <TSU1>  
A:Cross-references: GB:U52074; NID:91326148; PIDN:AAB40903.1; PID:91326149

A:Accession: PC4315  
A:Molecule type: protein  
A:Residues: 37-43;142-148 <TSU2>  
C:Comment: This receptor is involved in the initial adhesive interaction between lymph  
sites of inflammation.  
C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology  
F:1-38/Domain: signal sequence #status predicted <SIG>  
F:39-372/Product: L-selectin #status predicted <MNT>  
F:39-372/Product: L-selectin #status predicted <MNT>  
F:160-191/Domain: EGF homology <EGF>  
F:197-254/Domain: complement factor H repeat homology <FHL>  
F:259-316/Domain: complement factor H repeat homology <FHL>  
F:333-355/Domain: transmembrane #status predicted <TM>  
F:356-372/Domain: intracellular #status predicted <INT>

Query Match 94.1%; Score 1992; DB 2; Length 372;  
Best Local Similarity 93.5%; Pred. No. 1e-140;  
Matches 348; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

QY 1 MIFPMKOSTORDLNMIFKLMGWTMLCCDFLAHHGTCWTHYSEKPMNMOARRECRDN 60  
|||||  
DB 1 MIFPMKOSTORDLNMIFKLMGWTMLCCDFLAHHGTCWTHYSEKPMNMOARRECRDN 60  
|||||

QY 61 YTDLVAIONKAEIYELEKTLPEFSRSYWIIGIRKIGITWVGINKSLTEAEENMGDGEPN 120  
|||||  
DB 61 YTDLVAIONKAEIYELEKTLPEFSRSYWIIGIRKIGITWVGINKSLTEAEENMGDGEPN 120  
|||||

QY 121 NKKNKEDCEVEIYIKRNKADAGKNDACHKRLKALCYTASCPWSCSGHGECEVEIINNHTC 180  
|||||  
DB 121 NKKNKEDCEVEIYIKRNKADAGKNDACHKRLKALCYTASCPWSCSGHGECEVEIINNHTC 180  
|||||

QY 181 NCDVGYGPOQOLVIOCEPLEAPELGTMCTHPFGNFSFSQCAFSCSEGNLTGIEETT 240  
|||||  
DB 181 NCDVGYGPOQOLVIOCEPLEAPELGTMCTHPFGNFSFSQCAFSCSEGNLTGIEETT 240  
|||||

QY 241 CGPFGNMSSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTSACTFCSEGTTELIGKK 300  
|||||  
DB 241 CGPFGNMSSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTSACTFCSEGTTELIGKK 300  
|||||

QY 301 TICSSGIMSNPSPICQKLDKSFMSIKEGDYNPFLTIPVAVMTAFSGLAFTIIMLARLKK 360  
|||||  
DB 301 TICSSGIMSNPSPICQKLDKSFMSIKEGDYNPFLTIPVAVMTAFSGLAFTIIMLARLKK 360  
|||||

QY 361 GKSKRSMDPY 372  
|||||  
DB 361 GKSKRSMDPY 372  
|||||

RESULT 3  
JC4892  
L-selectin precursor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 21-Jan-2000  
C:Accession: JC4892  
R:Qian, J.; Huang, X.; Marks, R.M.  
A:Title: Cloning of the cDNA for rabbit L-selectin and expression of recombinant prot  
A:Reference number: JC4892; MUID:96354800  
A:Accession: JC4892  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-376 <QIA>  
A:Cross-references: GB:U26535; NID:9847787; PIDN:AAA67896.1; PID:9847788  
C:Comment: This protein involved in leukocyte-endothelial adhesion; it mediates adhes  
C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology  
F:1-37/Domain: signal sequence #status predicted <SIG>  
F:29-155/Domain: C-type lectin homology <LCH>  
F:38-376/Product: L-selectin #status predicted <MNT>  
F:160-191/Domain: EGF homology <EGF>  
F:197-254/Domain: complement factor H repeat homology <FHL>  
F:259-316/Domain: complement factor H repeat homology <FHL>



```

Query Match 84.9%: Score 1796; DB 2; Length 376;
Best Local Similarity 84.1%: Pred. No. 3,6e-126;
Matches 311; Conservative 24; Mismatches 35; Indels 0; Gaps 0;

Oy 1 MIFPKKCSOTQPDNLNIFKLMGWTMLCCDFLAHGGTYCMTYHSEKPMNQARARFECRDN 60
Db 1 MIFPKKCSPOGLGNVNFYFLMWTATLCCDFLAHGNINCTYHSEKPMNERARKFEREN 60
Oy 61 YTDLVAIQKAEIYLEKTLPLFSRSYYWIGIRKIGGIWTVGNTKSLTEBAENMGDEPN 120
Db 61 YTDLVAIQKGEIYLEKTLPLFSRSYYWIGIRKIGNIMTVGNTKSLTAEAEENMGDEPN 120
Oy 121 MKKNNEDCEYIITKRKKDAGKNNDDACIKLKAALCTTASQPMSCSGHGCVETLINHTC 180
Db 121 NKTTEDECEYIITKRRLDRGKNNDDSCQRKALCTTASCHPGSCSHGCVETINNYTC 180
Oy 181 NCDVGYGGQCOLVIOCEPLLEAPELCTMDCTHPGNGNFSFGCAFSCSEETNLTGIEET 240
Db 181 SCDVGYGGQCOLVIOCEPLLEAPELCTMDCTHPGNGNFSFGCAFSCSEETNLTGIEET 240
Oy 241 CGPFGNWSPEPTCOYIOCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGETLIGKK 300
Db 241 CGPLGNWSLRLPTCOYIOCEPLTAPDLGTDCSHPRAVFGFTSTCFPSCEGALLIGKK 300
Oy 301 TTCSSGIMTNSNPICQIKDKFSMTKEGDYNFLFPVAVMTAFSGLATIWLARLKK 360
Db 301 TVCGSSGIMSSPTPKQKVDRSFSMIKEGDYNFLFPVAVMTAFSGLATIWLARLKK 360
Oy 361 GKSKRSKMD 370
Db 361 GKSKRSKDD 370

RESULT 4
S22124
L-selectin precursor - bovine
N:Alternate names: Leucocyte cell adhesion molecule 1 (LECAM-1)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revisions 21-Feb-1995 #text_change 21-Jan-2000
C:Accession: S22124; A46531
R:Bosworth, B.T.
submitted to the EMBL Data Library, October 1991
A:Reference number: S22123
A:Accession: S22124
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-370 <BOS>
A:Cross-references: EMBL:X62882; NID:9515; PID:CA44676.1; PID:9516
R:Walcheck, B.; White, M.; Kurk, S.; Kishimoto, T.K.; Jutila, M.A.
Eur. J. Immunol. 22, 469-476, 1992
A:Title: Characterization of the bovine peripheral lymph node homing receptor: a lectin
A:Reference number: A46531; MUID:92164727
A:Accession: A46531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 39-79, 'Q', 81-151, 'K' <MAL>
A:Note: sequence inconsistent with the nucleotide translation
C:Superfamily: L-selectin, C-type lectin backbone (NCBIN:85686, NCARP:85687)
F:29-155/Domain: C-type lectin homology <LCH>
F:160-191/Domain: EGF homology <EGF>
F:197-254/Domain: complement factor H repeat homology <FH1>
F:259-316/Domain: complement factor H repeat homology <FH2>

Query Match 79.5%: Score 1682; DB 2; Length 370;
Best Local Similarity 77.0%: Pred. No. 1e-117;
Matches 282; Conservative 42; Mismatches 40; Indels 2; Gaps 1;

Oy 1 MIFPKKCSOTQPDNLNIFKLMGWTMLCCDFLAHGGTYCMTYHSEKPMNQARARFECRDN 60
Db 1 MIFPKKCSPOGLGNVNFYFLMWTATLCCDFLAHGNINCTYHSEKPMNERARKFEREN 60
Oy 61 YTDLVAIQKAEIYLEKTLPLFSRSYYWIGIRKIGGIWTVGNTKSLTEBAENMGDEPN 120
Db 61 YTDLVAIQKGEIYLEKTLPLFSRSYYWIGIRKIGNIMTVGNTKSLTAEAEENMGDEPN 120
Oy 121 MKKNNEDCEYIITKRKKDAGKNNDDACIKLKAALCTTASQPMSCSGHGCVETLINHTC 180
Db 121 NKTTEDECEYIITKRRLDRGKNNDDSCQRKALCTTASCHPGSCSHGCVETINNYTC 180
Oy 181 NCDVGYGGQCOLVIOCEPLLEAPELCTMDCTHPGNGNFSFGCAFSCSEETNLTGIEET 240
Db 181 SCDVGYGGQCOLVIOCEPLLEAPELCTMDCTHPGNGNFSFGCAFSCSEETNLTGIEET 240
Oy 241 CGPFGNWSPEPTCOYIOCEPLSAPDLGIMNCSHPLASFSFTSACTFICSEGETLIGKK 300
Db 241 CGPLGNWSLRLPTCOYIOCEPLTAPDLGTDCSHPRAVFGFTSTCFPSCEGALLIGKK 300
Oy 301 TTCSSGIMTNSNPICQIKDKFSMTKEGDYNFLFPVAVMTAFSGLATIWLARLKK 360
Db 301 TVCGSSGIMSSPTPKQKVDRSFSMIKEGDYNFLFPVAVMTAFSGLATIWLARLKK 360
Oy 361 GKSKRSKMD 370
Db 361 GKSKRSKDD 370

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Db      1  MLCMKKQQAQAGLGNVNEFLWVIMLCQDFEHHGHTDCWFHYHSKRPRPWKEARFACEN  60
Qy      61  YTDLVAIQKAEIYLEKTLTPFSRSYWIIGIRKIGGIWTWGTNKSLTLEAEVNMGDGEPN  120
Db      61  YTDLVAIQKGEIILEKTLTPFSRTYWIIGIRKYGVTWGTNKSLTLEAEVNMGDGEPN  120
Qy      121  NKKNKEDCEVEITYIKRNKQAGKWNDDACHKRLKALCYTASQWSSGSGEGVEIINNHTC  180
Db      121  NKKSKEDCEVEITYIKRNKSGKWNDDACHKAKATALCYTASCKWSSGSGGQCEVINNYTC  180
Qy      181  NCDVGYGQCQCLVIOCEPLLEAPELGTMDCTHPFCNFSFSSQCAFCSEGTNLTIIEET  240
Db      181  NCDLGTGYGECQFVYQCPLEAPKLTGMACHTRPCNFSFMSQCAFCNCKGDMICVEETT  240
Qy      241  CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSFTSACTFTCSGTELDIGKK  300
Db      241  CAPFGNWSPEPTCHVIOCEPLTEPDLDGMDCNHDLVDGFFSSTCTFCSEAEELTGKK  300
Qy      301  TICGSSGIMSNSPICQKLDKFSMKEGDYRPLFIPAAYWVTAISGLAFIIMLARLKK  360
Db      301  TICGSLSGMNSPSPICQKINRTISINESDYNPLFIPAAYWVTAISGLAFIIMLARLK  359
Qy      361  GKSKR 366
Db      360  -RKSCK 364

RESULT  5
S23936
L-selectin precursor - rat
M:Alternate names: leucocyte cell adhesion molecule 1 (LECAM-1)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 20-Jun-2000
C:Accession: S23936
R:Tatanebe, T.; Song, Y.; Hirayama, Y.; Tamateani, T.; Kulda, K.; Miyasaka, M.
Biochim. Biophys. Acta 1131, 321-324, 1992
A:Title: Sequence and expression of a rat cDNA for LECAM-1.
A:Reference number: S23936; MUID:92329548
A:Accession: S23936
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-372 <Mat>
A:Cross-References: GB:010831; NID:g220801; PIDN:BA01613.1; PID:g220802
C:Superfamily: L-selectin; C-type lectin homology; complement factor H repeat homology
C:Keywords: transmembrane protein
F:29-155/Domain: C-type lectin homology <LCH>
F:160-191/Domain: EGF homology <EGF>
F:197-254/Domain: complement factor H repeat homology <FH>
F:259-316/Domain: complement factor H repeat homology <FH2>

Query Match      78.1%  Score 1653; DB 2; Length 372;
Best Local Similarity 76.9%  Pred. No. 1.5e-115;
Matches 286; Conservative 35; Mismatches 51; Indels 0; Gaps 0;

Qy      1  MLEPWKCOSTORDLNIKFLMGWMLACDPLAHNGTCMYTHYSEKPMNOMORARFCRDN  60
Db      1  MVEFPRQSAQSGMSFLKWLIRTLCCDLLPHGTHCMTLHYHSRSMNWEARFCFHN  60
Qy      61  YTDLVAIQKAEIYLEKTLTPFSRSYWIIGIRKIGGIWTWGTNKSLTLEAEVNMGDGEPN  120
Db      61  YTDLVAIQNKREIYLEKTLTPKNPYWYWIIGIRKIGKWTWGTNKTLEKAEENMOTGEPN  120
Qy      121  NKKNKEDCEVEITYIKRNKQAGKWNDDACHKRLKALCYTASQWSSGSGEGVEIINNHTC  180
Db      121  NKKSKEDCEVEITYIKRERSGKWNDDACHKRAALCYTASQPESCNRRGECVEITINNHTC  180
Qy      181  NCDVGYGQCQCLVIOCEPLLEAPELGTMDCTHPFGNFSFSSQCAFCSEGTNLTIIEETT  240
Db      181  ICDPEYTYGQCQYVIOCEPLKAPELGTIMNCJHPGDSFQGCQCAFCNCGSEGLGMAKTE  240
Qy      241  CGPFGNWSPEPTCOVIOCEPLSAPDLGIMNCSHPLASFSFTSACTFTCSGTELDIGKK  300
Db      1  MLCMKKQQAQAGLGNVNEFLWVIMLCQDFEHHGHTDCWFHYHSKRPRPWKEARFACEN  60

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121	NKKNNEDCVELIYIRNRNDAGKMNDDCAHKIKALCTYACQPMWSSGGEGCEVETIINHTC	180
122	NKKNNEDCVELIYIRNRNDAGKMNDDCAHKIKALCTYACQPMWSSGGEGCEVETIINHTC	181
123	NKKNNEDCVELIYIRNRNDAGKMNDDCAHKIKALCTYACQPMWSSGGEGCEVETIINHTC	182
124	NKKNNEDCVELIYIRNRNDAGKMNDDCAHKIKALCTYACQPMWSSGGEGCEVETIINHTC	183
125	NKKNNEDCVELIYIRNRNDAGKMNDDCAHKIKALCTYACQPMWSSGGEGCEVETIINHTC	184
126	NKKNNEDCVELIYIRNRNDAGKMNDDCAHKIKALCTYACQPMWSSGGEGCEVETIINHTC	185
127	NKKNNEDCVELIYIRNRNDAGKMNDDCAHKIKALCTYACQPMWSSGGEGCEVETIINHTC	186
128	NKKNNEDCVELIYIRNRNDAGKMNDDCAHKIKALCTYACQPMWSSGGEGCEVETIINHTC	187
129	NKKNNEDCVELIYIRNRNDAGKMNDDCAHKIKALCTYACQPMWSSGGEGCEVETIINHTC	188
130	NKKNNEDCVELIYIRNRNDAGKMNDDCAHKIKALCTYACQPMWSSGGEGCEVETIINHTC	189
131	NCDVGYIYAPCOQLYIOCEPLDAPBLGTMDCTPFGNFSFSSOCASFSGEGLNLGTIEPT	240
132	NCDVGYIYAPCOQLYIOCEPLDAPBLGTMDCTPFGNFSFSSOCASFSGEGLNLGTIEPT	241
133	NCDVGYIYAPCOQLYIOCEPLDAPBLGTMDCTPFGNFSFSSOCASFSGEGLNLGTIEPT	242
134	NCDVGYIYAPCOQLYIOCEPLDAPBLGTMDCTPFGNFSFSSOCASFSGEGLNLGTIEPT	243
135	NCDVGYIYAPCOQLYIOCEPLDAPBLGTMDCTPFGNFSFSSOCASFSGEGLNLGTIEPT	244
136	NCDVGYIYAPCOQLYIOCEPLDAPBLGTMDCTPFGNFSFSSOCASFSGEGLNLGTIEPT	245
137	NCDVGYIYAPCOQLYIOCEPLDAPBLGTMDCTPFGNFSFSSOCASFSGEGLNLGTIEPT	246
138	NCDVGYIYAPCOQLYIOCEPLDAPBLGTMDCTPFGNFSFSSOCASFSGEGLNLGTIEPT	247
139	NCDVGYIYAPCOQLYIOCEPLDAPBLGTMDCTPFGNFSFSSOCASFSGEGLNLGTIEPT	248
140	NCDVGYIYAPCOQLYIOCEPLDAPBLGTMDCTPFGNFSFSSOCASFSGEGLNLGTIEPT	249

61 YTDVAIQNAKEIYELEKTLPEFSRSYIYGIRKIGGIWTVGCTNKSLEAEENMGDGBPN 120

```

Db 61 YTDVAIONKKEIEYLEFTLPKSPYYWIGIRKIGKMTWGTNTLTKEAENMGAGEPN 120
      ||||||| ||||| ||| ||||||| :|||||:||||| |||
Qy 121 NKKNEDEVEIYIKRNKDGKMNDDACHKRLKAALCYTASQPMSCSGHECEVEIINNHTC 180
      |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 NKKKEDEVEIYIKRERSGKMNDDACHKRAALCYTASQPGSCNGGECVEITINNHTC 180
Qy 181 NCDVYGYGPOQOLVIOCEPLAEPBLGTMDCTHPFGNFSFSSQCAFSCEGTLGIEETT 240
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ICDAGYGVPOQOYVQCERPLAEPBLGTMDCIHPLGNFSFGSCAFNCSGRELGTAEI 240
Qy 241 CGPFGNMSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTACTFICSSETELGKKK 300
      ||| ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 CGASGNMSPPEPTCOVQVOCPEPLAEPBLGTMDCIHPLGNFSFGSCAFNCSGRELGTAE 300
Qy 301 TTCSSGTSWNSPPICOKLDKFSMIRKEDYNPLETIPAAVWTAFAAGLFIIMLARLKK 360
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TQCGASGNMSPPEPTCOETNFSFKIKEDYNPLETIPAAVWTAFAAGLFIIMLARLKK 360
Qy 361 GKSKRSMDPY 372
      ||||| |||||
Db 361 GKSKERMDPY 372

RESULT 8
A30359
P-selectin precursor - human
N:Alternate names: CD62 antigen; granule membrane protein 140
C:Species: Homo sapiens (man)
C>Date: 18-Oct-1989 #sequence_rev1sion 30-Sep-1991 #text_change 19-May-2000
C:Accession: A30359
R:Johnson, G.I.; Cook, R.G.; McEver, R.P.
Cell 56, 1033-1044, 1989
A:Title: Cloning of GMP-140, a granule membrane protein of platelets and endothelium: se
A:Reference number: A30359; MUID:89166432
A:Accession: A30359
A:Molecule type: mRNA
A:Residues: 1-830 <JOH>
A:Cross-references: GB:M25322
A>Note: parts of this sequence, including the amino end of the mature protein, were cont
A:Genetics:
A:Gene: GDB:SELP; GRMP
A:Cross-references: GDB:120018; OMIM:173610
A:Map position: 1q22-1q25
C:Superfamily: unassigned EGF-related proteins; complement factor H repeat homology; EGF
C:Keywords: cell adhesion; glycoprotein; phosphohistidine; phosphoprotein; surface anti
F:1-41/Domain: signal sequence #status predicted <SIG>
F:42-830/Product: P-selectin #status experimental <MAT>
F:163-194/Domain: EGF homology <EGF>
F:200-257/Domain: complement factor H repeat homology <FH01>
F:262-319/Domain: complement factor H repeat homology <FH02>
F:324-381/Domain: complement factor H repeat homology <FH03>
F:386-443/Domain: complement factor H repeat homology <FH04>
F:448-505/Domain: complement factor H repeat homology <FH05>
F:510-567/Domain: complement factor H repeat homology <FH06>
F:572-629/Domain: complement factor H repeat homology <FH07>
F:642-699/Domain: complement factor H repeat homology <FH08>
F:704-761/Domain: complement factor H repeat homology <FH09>
F:772-795/Domain: transmembrane #status predicted <TM>
F:796-830/Domain: intracellular #status predicted <CY>
F:54,98,180,212,219,411,460,518,665,716,723,741/Binding site: carbohydrate (Asn) (cova

```

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Db 71 QNKNEIDYLNKVLPPYSSYWIIGIRKNNKMTWGTGKALINEAENMADNEPNKRNED 130
Qy 128 CVEIYIKRNKDGKMNDDACHKRLKAALCYTASQPMSCSGHECEVEIINNHTCNDVGY 187
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 CVEIYIKRSPASAGKMNDDACHKRLKALCYTASQPMSCSGKQCELETTIGNYTCSPGY 190
Qy 188 GPQOLVIOCEPLAEPBLGTMDCTHPFGNFSFSSQCAFSCEGTLGIEETTGPFGNW 247
      |||: ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 191 GPECEYVRECGELTLPQVHVLNMCNSHPLCNFNSQCSFHCFTDGVNPSKLECLASGIW 250
Qy 248 SSPEPTCOVIOCEPLASAPDLGIMNCSHPLASFSTACTFICSSETELGKKKTTCESSG 307
      |||: ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 251 TNKPQOCLAACPPLKIPERNMTCIHSAKAFQHSQCSFSCSEGFALVGEVWQCTASG 310
Qy 308 IWSNPSICO 317
      |||: ||| |||||
Db 311 VWTAPAPYCK 320

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RESULT 9
A42755
P-selectin precursor - mouse
N:Alternate names: CD62; granule membrane protein 140; PADGEM
C:Species: Mus musculus (house mouse)
C>Date: 04-Mar-1993 #sequence_rev1sion 18-Nov-1994 #text_change 19-May-2000
C:Accession: A42755; A44899
R:Weller, A.; Isenmann, S.; Vestweber, D.
J. Biol. Chem. 267, 15176-15183, 1992
A:Title: Cloning of the mouse endothelial selectins. Expression of both E- and P-sele
A:Reference number: A42755; MUID:92340571
A:Accession: A42755
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-768 <WEL>
A:Cross-references: GB:M87861; NID:g200552; PIDN:AAA40008.1; PID:g200553
A:Experimental source: endothelial cells
A>Note: sequence extracted from NCBI backbone (NCBI:P:109467)
R:Sanders, W.E.; Wilson, R.W.; Ballantyne, C.M.; Beaudet, A.L.
Blood 80, 795-800, 1992
A:Title: Molecular cloning and analysis of in vivo expression of murine P-selectin.
A:Reference number: A44899; MUID:92345617
A:Accession: A44899
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-723, 'F', 725-768 <SAN>
A:Cross-references: GB:M72332; NID:g193565; PIDN:AAA37712.1; PID:g193566
A>Note: sequence extracted from NCBI backbone (NCBI:P:109900)
C:Superfamily: unassigned EGF-related proteins; complement factor H repeat homology;
C:Keywords: cell adhesion; glycoprotein; phosphohistidine; phosphoprotein; transmembr
F:1-41/Domain: signal sequence #status predicted <SIG>
F:42-768/Product: P-selectin #status predicted <MAT>
F:163-194/Domain: EGF homology <EGF>
F:200-257/Domain: complement factor H repeat homology <FH01>
F:262-319/Domain: complement factor H repeat homology <FH02>
F:324-381/Domain: complement factor H repeat homology <FH03>
F:386-443/Domain: complement factor H repeat homology <FH04>
F:448-505/Domain: complement factor H repeat homology <FH05>
F:510-567/Domain: complement factor H repeat homology <FH06>
F:580-637/Domain: complement factor H repeat homology <FH07>
F:642-699/Domain: complement factor H repeat homology <FH08>
F:710-733/Domain: transmembrane #status predicted <TM>
F:734-768/Domain: intracellular #status predicted <INT>
F:45,54,107,212,347,398,456,467,603,654,661,679/Binding site: carbohydrate (Asn) (cov

```

```

Query Match 42.8%; Score 905; DB 2; Length 830;
Best Local Similarity 50.6%; Pred. No. 1,1e-59;
Matches 157; Conservative 47; Mismatches 106; Indels 0; Gaps 0;
Qy 8 OSTRODLWNIFKMGWMLCDPLAHIGTYCWTYHSEKPMNQRARFCRDNTDLVAI 67
      |||: ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11 QREFRVAVFGISQLCFSLISELTNOKEVAAWTHYTKAVSWINSRKYCONRTDLVAI 70
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 68 QNKAIEYLEKTELPFSRSYWIIGIRKIGTITWVTGNTSLTEAENMGDEPNKKKED 127
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Query Match 42.7%; Score 902.5; DB 2; Length 768;
Best Local Similarity 52.0%; Pred. No. 1,1e-59;
Matches 156; Conservative 40; Mismatches 103; Indels 1; Gaps 1;
Qy 20 LMGWMLCDPLAHIGTYCWTYHSEKPMNQRARFCRDNTDLVAIONKAIEYLEKT 79
      |||: ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 24 IW-FSALISELVNOKEVAAWTHYTKAVSWINSRVFCRHFTDLVAIONKNEIHLMDV 82
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



A:Reference number: A35046; MUID:90175359  
A:Accession: A35046  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-610 <HES>  
A:Cross-references: GB:M0640; NID:g182047; PIDN:AAA52377.1; PID:g182048  
R:Revellacqua, M.P.; Scengellari, S.; Gimbrone Jr., M.A.; Seed, B.  
Science 243, 1160-1165, 1989  
A>Title: Endothelial leukocyte adhesion molecule 1: an inducible receptor for neutrophils  
A:Reference number: A32606; MUID:89162047  
A:Accession: A32606  
A:Molecule type: mRNA  
A:Residues: 1'467,'Y',469-610 <BEV>  
A:Cross-references: GB:M24736; NID:g537523; PIDN:AAA52376.1; PID:g537524  
C:Genetics:  
A:Gene: GDB:SELE; ELAM; ESEL; ELAMI  
A:Cross-references: GDB:I20612; OMIM:131210  
A:Map position: 1q22-1q25  
C:Superfamily: unassigned EGF-related proteins; C-type lectin homology; complement factor  
C:Keywords: duplication; glycoprotein; tandem repeat; transmembrane protein  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:12-138/Domain: C-type lectin homology <LCH>  
F:22-610/Product: endothelial leukocyte adhesion molecule 1 #status predicted <MAT>  
F:143-114/Domain: EGF homology <EGF>  
F:180-237/Domain: complement factor H repeat homology <FH01>  
F:242-299/Domain: complement factor H repeat homology <FH02>  
F:304-362/Domain: complement factor H repeat homology <FH03>  
F:367-425/Domain: complement factor H repeat homology <FH04>  
F:430-488/Domain: complement factor H repeat homology <FH05>  
F:493-547/Domain: complement factor H repeat homology <FH06>  
F:557-578/Domain: transmembrane #status predicted <TM>  
F:25,145,160,179,199,203,265,312,332,503,527/Binding site: carbohydrate (Asn) (covalently

```

QY 270 MNCSHPLASFSTSACTFICSETELIGKKKTTICSSGIWSPSPICQ 317
      || : : : ||| | || : : | |||| | : | :
Db 261 RKCSSNPGSYPWNNTCTCTFDCVEGYRRVGAQNLQCTSSGIWDNETPSC 308

```

	Query Match	40.5%;	Score 857;	DB 2;	Length 618;
	Best Local Similarity	51.4%;	Pred. No 3e-56;		
	Matches 148;	Conservative 42;	Mismatches 96;	Indels 2;	Gaps 2;
QY	31 LAHHGTCVMTYHYSEKPMNORARFCRDNYTDLVAIONKAEILEYKLTPEFSNSYWG	90			
Db	22 LAGEST-AMYNASSELMTYDEASAYCORYDTHLVAIONKEEILYLSNLSKHSPTYWIG	80			
QY	91 IRKGGIWTWGTGTRKSLTEEAENGDEGPNNKKKEPCVEEYIKRNNDACKWMDCHKL	150			
Db	81 IRKYNWNWIVWGTRKPLETEENQNNARPEPNNKKQNEECVEIYIORTKDSMMNDERCNKK	140			
QY	151 KALCTYASCOPMSCSGHGECVELIINNHTGNCVDYGYGPOCOLVIOCEPLDABELGTMDC	210			
Db	141 KIALCTYASTNASCSGHGECIEIINSYTCCKHPGFGAPMCDEQAVTCKPQHPHDYGLNC	200			
QY	211 THPEGNFSYSCAFSCSEGNLTGIEET-CCGFFGWMSSPEPTCOYIOCEPLSADPLGI	269			
Db	201 SHPEGPFYSYSCSGFGCKRGRLTSSMETTYRCTSSGWSMSPACACHVECEALTHPAHG	260			

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: January 13, 2001, 01:14:47 ; Search time 32.92 Seconds

(without alignments)  
364.927 Million cell updates/sec

Title: US-09-119-209-2

Perfect score: 2116

Sequence: 1 MFPWKQSTORDLNIFKL.....MLARRLKKGKSKRSMNDPY 372

Scoring table: BLASTSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Length	ID	Description
1	2090	98.8	372 1	LEM1_HUMAN
2	2085	98.5	372 1	LEM1_PANTR
3	2062	97.4	372 1	LEM1_PONPY
4	1996	94.3	372 1	LEM1_MACMU
5	1992	94.1	372 1	LEM1_PAPHA
6	1682	79.5	370 1	LEM1_BOVIN
7	1653	78.1	372 1	LEM1_RAT
8	1651	78.0	372 1	LEM1_MOUSE
9	919.5	43.5	769 1	LEM3_SHEEP
10	905	42.8	830 1	LEM3_HUMAN
11	902.5	42.7	768 1	LEM3_MOUSE
12	894.5	42.3	646 1	LEM3_BOVIN
13	885	41.8	768 1	LEM3_RAT
14	862	40.7	610 1	LEM2_HUMAN
15	861	40.7	551 1	LEM2_RABIT
16	860	40.6	611 1	LEM2_CANFA
17	858.5	40.6	549 1	LEM2_RAT
18	857	40.5	612 1	LEM2_MOUSE
19	849.5	40.1	485 1	LEM2_BOVIN
20	814.5	38.5	484 1	LEM2_PIG
21	212.5	10.0	1019 1	LEM2_TACTR
22	199.5	9.4	1231 1	CEAH_HUMAN
23	195	9.2	958 1	HIG_DROME
24	189.5	9.0	1019 1	LFC_CARRO
25	172	8.1	2039 1	CRI_HUMAN
26	171	8.1	564 1	PGCA_CANFA
27	168	7.9	2132 1	PGCA_MOUSE
28	167	7.9	321 1	FCE2_HUMAN
29	167	7.9	1234 1	CEAH_MOUSE
30	166.5	7.9	558 1	CABP_RAT
31	166	7.8	390 1	DAFI_MOUSE
32	166	7.8	1456 1	MANR_HUMAN
33	166	7.8	2364 1	PGCA_BOVIN

34	165	7.8	311 1	LECI_HUMAN	P07307 homo sapien
35	165	7.8	548 1	KUCR_MOUSE	P70194 mus musculus
36	163	7.7	2124 1	PGCA_RAT	P07897 rattus norv
37	162.5	7.7	345 1	APDH_BOVIN	P17690 bos taurus
38	162	7.7	304 1	MGML_MOUSE	P49300 mus musculus
39	160	7.6	2415 1	PGCA_HUMAN	P16112 homo sapien
40	157	7.4	331 1	FCE2_MOUSE	P20693 mus musculus
41	157	7.4	469 1	CABP_MOUSE	P08607 mus musculus
42	157	7.4	610 1	CABP_BOVIN	P02805 bos taurus
43	156.5	7.4	207 1	LECH_CHICK	P02707 gallus gal
44	156.5	7.4	1025 1	CR2_MOUSE	P19070 mus musculus
45	156	7.4	258 1	CABP_RAT	Q63515 rattus norv

## ALIGNMENTS

RESULT	ID	LEM1_HUMAN	STANDARD:	PRT:	372 AA.
AC	PI4151	PI5023			
DT	01-JAN-1990	(rel. 13, Created)			
DT	01-FEB-1991	(rel. 17, Last sequence update)			
DT	30-MAY-2000	(rel. 39, Last annotation update)			
DE	L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (T01) (GP90-MEL)				
DE	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).				
DE	SELL OR LYAM1 OR LNHK.				
CN	Homo sapiens (Human).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89315837; PubMed=2664786;				
RA	Siegelman M.H., Weissman I.L.;				
RT	"Human homologue of mouse lymph node homing receptor: evolutionary conservation at tandem cell interaction domains.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 86:5562-5566(1989).				
RL	[2]				
RN	SEQUENCE FROM N.A.				
RP	TISSUE=TONSIL;				
RC	MEDLINE=89310350; PubMed=2473156;				
RX	Tedder T.F., Isaacs C.M., Ernst T.J., Demetri G.D., Adler D.A.,				
RA	Distriche C.M.;				
RT	"Isolation and chromosomal localization of cDNAs encoding a novel human lymphocyte cell surface molecule, LAM-1. Homology with the mouse lymphocyte homing receptor and other human adhesion proteins.";				
RT	J. Exp. Med. 170:123-133(1989).				
RL	[3]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=90044046; PubMed=2509939;				
RX	Camerini D., James S.P., Stamenkovic I., Seed B.;				
RA	"Leu-8/T01 is the human equivalent of the Mel-14 lymph node homing receptor.";				
RT	Nature 342:78-82(1989).				
RL	[4]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=89308881; PubMed=2663882;				
RX	Bowen B.R., Nguyen T., Lasky L.A.;				
RA	"Characterization of a human homologue of the murine peripheral lymph node homing receptor.";				
RT	J. Cell Biol. 109:421-427(1989).				
RL	[5]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=90243637; PubMed=1692315;				
RX	Ord D.C., Ernst T.J., Zhou L.J., Rambaldi A., Spectral O.,				
RA	Griffin J., Tedder T.F.;				
RT	"Structure of the gene encoding the human leukocyte adhesion molecule-1 (T01, Leu-8) of lymphocytes and neutrophils.";				
RT	J. Biol. Chem. 265:7760-7767(1990).				
RL	-1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIANE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.				
CC					

Query Match	Best Local Similarity	Score	DB 1;	Length	372;
Matches	368;	Conservative	1;	Mismatches	35;
				Indels	0;
				Gaps	0;
FT CARBOHYD	232	232	N-LINKED (GLCNAC. . .)	(POTENTIAL)	
FT CARBOHYD	246	246	N-LINKED (GLCNAC. . .)	(POTENTIAL)	
FT CARBOHYD	271	271	N-LINKED (GLCNAC. . .)	(POTENTIAL)	
FT CARBOHYD	311	311	N-LINKED (GLCNAC. . .)	(POTENTIAL)	
FT CONFLICT	37	37	D -> Y (IN REF. 4).		
FT CONFLICT	178	178	Y -> H (IN REF. 4).		
FT CONFLICT	193	193	F -> S (IN REF. 1 AND 4).		
FT CONFLICT	213	213	P -> S (IN REF. 3).		
FT CONFLICT	214	214	L -> F (IN REF. 4).		
FT CONFLICT	218	220	SFS -> MFN (IN REF. 2).		
FT CONFLICT	242	242	G -> E (IN REF. 2).		
SQ SEQUENCE	372 AA;	42187 MW;	6EA9918EACA2D3643	CNC64;	
Query Match	98.8%;	Score 2090;	DB 1;	Length 372;	
Best Local Similarity	98.9%;	Pred. No. 1,66-158;			
Matches 368;	Conservative	1;	Mismatches	35;	
			Indels	0;	
			Gaps	0;	
QY 1 MIEPMKOSTORDLNNIFKLMGTMLCODFLAHGTQMTYHYSKPPNNQRRARFCRDN 60					
Db 1 MIEPMKOSTORDLNNIFKLMGTMLCODFLAHGTQMTYHYSKPPNNQRRARFCRDN 60					
QY 61 YTDVAIQNKABIEYLEKTLPFSRSYWMIGIKIOGIMTWGTKNSLTEAENMGDEPN 120					
Db 61 YTDVAIQNKABIEYLEKTLPFSRSYWMIGIKIOGIMTWGTKNSLTEAENMGDEPN 120					
QY 121 NKKNKEDCEYIIRKNNKAGKWNDDACKKILKAALCYTASCPWSCSGHGEVCELINNHTC 180					
Db 121 NKKNKEDCEYIIRKNNKAGKWNDDACKKILKAALCYTASCPWSCSGHGEVCELINNHTC 180					
EY 181 NCDVGYGPOCLVYOCPEPLLEAPLELGTMDCTHPFGNFSFSSQCAFSSSEGNLTGIRETT 240					
Db 181 NCDVGYGPOCLVYOCPEPLLEAPLELGTMDCTHPFGNFSFSSQCAFSSSEGNLTGIRETT 240					
QY 241 CGPFGNMSSPEPTQCYIOCEPLSAPDLGICINMCSHPPLASFSTSACTICSEGTIELIGKKK 300					
Db 241 CGPFGNMSSPEPTQCYIOCEPLSAPDLGICINMCSHPPLASFSTSACTICSEGTIELIGKKK 300					
QY 301 TICESSGIWSNPSPICOKLDFKFSMIKRGDYNPLFIYAAVVAWTAFSGLAFTIMLARLKK 360					
Db 301 TICESSGIWSNPSPICOKLDFKFSMIKRGDYNPLFIYAAVVAWTAFSGLAFTIMLARLKK 360					
QY 361 GKSKRSKSNDDY 372					
Db 361 GKSKRSKSNDDY 372					
RESULT 2					
LEML_PANTR	STANDARD;	PRT;	372 AA.		
AC 095237;					
DT 01-NOV-1997 (Rel. 35, Created)					
DT 01-NOV-1997 (Rel. 35, Last sequence update)					
DT 01-NOV-1997 (Rel. 35, Last annotation update)					
L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (C6b2L).					
DE					
GN					
OS Pan troglodytes (Chimpanzee).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.					
RA					
RA Bruman J.I., Fu H., Johnson C.E., Thakur A.B., Berg E.L.,					
RA Tsurushita N.					
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.					
CC - FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIANE THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL					
CC VENUES IN PERIPHERAL LYMPH NODES.					
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.					
CC - SIMILARITY: TO OTHER SELECTINS/LECAM.					
CC - SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.					
CC - SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.					



```

CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U73728; AAB18248.1; -.
DR HSSP: P14151; IKJB.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; lectin_C; 1.
DR PFAM: PF00084; sush1; 2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 355
FT DOMAIN 356 372
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT REPEAT 196 255
FT REPEAT 258 317
FT DISULFID 57 155
FT DISULFID 128 147
FT DISULFID 160 171
FT DISULFID 165 180
FT DISULFID 182 191
FT DISULFID 197 241
FT DISULFID 227 254
FT DISULFID 259 303
FT DISULFID 289 316
FT CARBOHYD 60 316
FT CARBOHYD 104 104
FT CARBOHYD 177 177
FT CARBOHYD 216 216
FT CARBOHYD 232 232
FT CARBOHYD 246 246
FT CARBOHYD 271 271
SO SEQUENCE 372 AA; 42188 MW; 6EA991802AD3643 CRC64;

Query Match 98.5% Score 2085; DB 1; Length 372;
Best Local Similarity 98.7% Pred. No. 3.9e-158;
Matches 367; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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DB 181 NCDVGYGQCFVIOCEPLAPLGTMDCTHPNLFNFSFSSOCARFSCSGTWTG1 EERT 240
OY 241 CGPFCNMWSPPEPTCOVIOCEPLASPDIGIMNCSHPLASFSFSACTFICSECTELIGKK 300
DB 241 CGPFCNMWSPPEPTCOVIOCEPLASPDIGIMNCSHPLASFSFSACTFICSECTELIGKK 300
OY 301 TFCSSGIMSNPSPIQOKKDKSFSM1KEGDYPLPTPAVAVWYAFSGLAFTIWLARRLKK 360
DB 301 TFCSSGIMSNPSPIQOKKDKSFSM1KEGDYPLPTPAVAVWYAFSGLAFTIWLARRLKK 360
OY 361 GKSKSRSMNDPY 372
DB 361 GKSKSRSMNDPY 372

RESULT 3
LEML_PONPY STANDARD: PRT: 372 AA.
ID LEML_PONPY
AC Q95235;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MOLECULE-1) (LAM-1) (LEUKOCYTE-HOMING RECEPTOR) (LEUKOCYTE ADHESION
DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1)
DE (LECAM1) (CD62L).
GN SELL.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
RN [1]
RP SEQUENCE FROM N.A.
RA Budman J.I., Fu H., Johnson C.E., Thakur A.B., Berg E.L.,
RA Tsurushita N.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHERENCE
CC OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL
CC VENULES IN PERIPHERAL LYMPH NODES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U73729; AAB18247.1; -.
DR HSSP: P14151; IKJB.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; lectin_C; 1.
DR PFAM: PF00084; sush1; 2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 355

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FT DOMAIN 356 372 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 35 155 C-TYPE LECTIN (SHORT FORM).
FT DOMAIN 156 192 EGF-LIKE.
FT DOMAIN 196 317 2 X SUSHI (SCR) REPEATS.
FT REPEAT 196 255 SUSHI 1.
FT REPEAT 258 317 SUSHI 2.
FT DISULFID 57 155 BY SIMILARITY.
FT DISULFID 128 147 BY SIMILARITY.
FT DISULFID 160 171 BY SIMILARITY.
FT DISULFID 165 180 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 197- 241 BY SIMILARITY.
FT DISULFID 227 254 BY SIMILARITY.
FT DISULFID 259 303 BY SIMILARITY.
FT DISULFID 289 316 BY SIMILARITY.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 372 AA: 42118 MW: 6517DD2213PF15E CRC64:

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Query Match 97.4%; Score 2062; DB 1; Length 372;
Best Local Similarity 97.6%; Pred. No. 2.6e-156;
Matches 363; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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QY 1 MIFPKCSTQDLDNIFLGMGTMLCDPFLAHGTCMTYHSKPKMQRARRFCNDN 60
DB 1 MIFPKCSTQDLDNIFLGMGTMLCDPFLAHGTCMTYHSKPKMQRARRFCNDN 60
QY 61 YTDVAIONKAEIYELEKTLFPRSRYWIGIRKIGITWGTNKSLEAEANMGDGPEN 120
DB 61 YTDVAIONKAEIYELEKTLFPRSRYWIGIRKIGITWGTNKSLEAEANMGDGPEN 120
QY 121 NKKNEDEVETIYKRNKAGKNDACKKLAALCYTASCPWSCSGHECEVEIINHTC 180
DB 121 NKKNEDEVETIYKRNKAGKNDACKKLAALCYTASCPWSCSGHECEVEIINHTC 180
QY 181 NCDVGYGPOGLVIOCEPLAPELGTMDCTHPFGNFSFSCAFSCSEGNLTGIEETT 240
DB 181 NCDVGYGPOGLVIOCEPLAPELGTMDCTHPFGNFSFSCAFSCSEGNLTGIEETT 240
QY 241 CGPFGNMSSPEPTCOVIOCEPLASAPDLGIMNCSPHLASFSTACTFICSGETELIGKK 300
DB 241 CGPFGNMSSPEPTCOVIOCEPLASAPDLGIMNCSPHLASFSTACTFICSGETELIGKK 300
QY 301 TICSSGIMWSPPICQKIDKSFMSIKEGDVNPLFIYAAVWVTFSGIAFLIWLARRLKK 360
DB 301 TICSSGIMWSPPICQKIDKSFMSIKEGDVNPLFIYAAVWVTFSGIAFLIWLARRLKK 360
QY 361 GKSKSRKSNDDPY 372
DB 361 GKSKSRKSNDDPY 372

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RESULT 4
LEML MACMU STANDARD: PRT: 372 AA.
AC 095198:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE I-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUCOCYTE ADHESION MOLECULE-1) (LAW-1) (LEUCOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
DE GN SEILL.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

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OC Cercopithecoidea; Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RA Budman J., Fu H., Johnson C.E., Thakur A.B., Berg E.L.,
RA Tsurushita N.
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHESION OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.
CC -! SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN.
CC -! SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -! SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -! SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -! SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS:
-----
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-----
CC EMBL: U73730; AB18246.1; -
DR HSSP: P14151; IKJB.
DR INTERPRO: IPR000436; -
DR INTERPRO: IPR000561; -
DR INTERPRO: IPR001304; -
DR INTERPRO: IPR002396; -
DR PRAM: PF00008; EGF_1.
DR PFAM: PF00059; lectin_c; 1.
DR PFAM: PF00084; sush1; 2.
DR PRINTS: PRO0343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS00041; C-TYPE_LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin; Selectin; Signal; Sush1; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 333 355 POTENTIAL.
FT DOMAIN 356 372 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 55 155 C-TYPE LECTIN (SHORT FORM).
FT DOMAIN 156 192 EGF-LIKE.
FT DOMAIN 196 317 2 X SUSHI (SCR) REPEATS.
FT REPEAT 196 255 SUSHI 1.
FT REPEAT 258 317 SUSHI 2.
FT DISULFID 57 155 BY SIMILARITY.
FT DISULFID 128 147 BY SIMILARITY.
FT DISULFID 160 171 BY SIMILARITY.
FT DISULFID 165 180 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 197 241 BY SIMILARITY.
FT DISULFID 227 254 BY SIMILARITY.
FT DISULFID 259 303 BY SIMILARITY.
FT DISULFID 289 316 BY SIMILARITY.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 372 AA: 42109 MW: 088D/DDS5C549D6D CRC64:

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Query Match 94.3%; Score 1996; DB 1; Length 372;
Best Local Similarity 93.8%; Pred. No. 4.4e-151;
Matches 349; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

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OY 1 MIEPMKCGSTQDLDNINIFKMGWMLCDFLAHGHGYCWTYHSEKPMNMQRARFCRDN 60
DB 1 MIEPMKCGSTQDLDNINIFKMGWMLCDFLAHGHGYCWTYHSEKPMNMQRARFCRDN 60
OY 61 YTDVAIQKAEIYELEKTLPPFSRSYWGIRKIGITWVGTNKSLEAEAMWGDGEPN 120
DB 61 YTDVAIQKAEIYELEKTLPPFSRSYWGIRKIGITWVGTNKSLEAEAMWGDGEPN 120
OY 121 NKKNKEDCEVEIYIKRNKDKGKNNDDACHKLAALCYTASQCPWSCSGHGECEVEIINNHTC 180
DB 121 NKKNKEDCEVEIYIKRNKDKGKNNDDACHKLAALCYTASQCPWSCSGHGECEVEIINNHTC 180
OY 181 NCDVGYGPOCQVIOCEPLLEAPBELGTMDCTHPFGNFSFSOCAPSCSEGTNLGIEETT 240
DB 181 NCDVGYGPOCQVIOCEPLLEAPBELGTMDCTHPFGNFSFSOCAPSCSEGTNLGIEETT 240
OY 241 CGPFGNWSSEPTTCOVIOCEPLSAPDLGIMNCSHPLASFSFSACFTFCSEGTNLGKRR 300
DB 241 CGPFGNWSSEPTTCOVIOCEPLSAPDLGIMNCSHPLASFSFSACFTFCSEGTNLGKRR 300
OY 301 TICSSGIMSNPSPIQCKLDRSFSMIKBDYDPLFIPVAVMTAFSGLAFTIWLARLKK 360
DB 301 TICSSGIMSNPSPIQCKLDRSFSMIKBDYDPLFIPVAVMTAFSGLAFTIWLARLKK 360
OY 361 GKSKRSMDPY 372
DB 361 GKSKRSMDPY 372
```

## RESULT 5

LEML\_PAPHA STANDARD: PRT: 372 AA.

AC 028768: 01-NOV-1997 (Rel. 35, Last Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

DE MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LRCAM1) (CD62L).

PFAM: PF00008; EGF\_1.  
PFAM: PF00059; lectin\_c\_1.  
PFAM: PF00084; sushi\_2.  
PRINTS: PR00343; SELECTIN.  
PROSITE: PS00022; EGF\_1; 1.  
PROSITE: PS01186; EGF\_2; 1.  
PROSITE: PS00615; C-TYPE LECTIN\_1; 1.  
PROSITE: PS00041; C-TYPE LECTIN\_2; 1.  
Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin; Selectin; Signal; Sushi; Repeat.

FT SIGNAL 1 28  
FT PROPEP 29 38  
FT CHAIN 39 372  
FT DOMAIN 39 332  
FT TRANSMEM 333 355  
FT DOMAIN 356 372  
FT DOMAIN 55 155  
FT DOMAIN 156 192  
FT DOMAIN 196 317  
FT REPEAT 196 255  
FT REPEAT 258 317  
FT DISULFID 57 155  
FT DISULFID 128 147  
FT DISULFID 160 171  
FT DISULFID 165 180  
FT DISULFID 182 191  
FT DISULFID 197 241  
FT DISULFID 227 254  
FT DISULFID 259 303  
FT DISULFID 289 316  
FT CARBOHYD 60 60  
FT CARBOHYD 104 104  
FT CARBOHYD 177 177  
FT CARBOHYD 226 226  
FT CARBOHYD 232 232  
FT CARBOHYD 246 246  
FT CARBOHYD 271 271  
SO SEQUENCE 372 AA; 42091 MW; 64E7BDD5AC549D69 CRC64;

Query Match 94.1%; Score 1992; DB 1; Length 372;

Best Local Similarity 93.5%; Pred. No. 9,1e-151;

Matches 348; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

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OY 1 MIEPMKCGSTQDLDNINIFKMGWMLCDFLAHGHGYCWTYHSEKPMNMQRARFCRDN 60
DB 1 MIEPMKCGSTQDLDNINIFKMGWMLCDFLAHGHGYCWTYHSEKPMNMQRARFCRDN 60
OY 61 YTDVAIQKAEIYELEKTLPPFSRSYWGIRKIGITWVGTNKSLEAEAMWGDGEPN 120
DB 61 YTDVAIQKAEIYELEKTLPPFSRSYWGIRKIGITWVGTNKSLEAEAMWGDGEPN 120
OY 121 NKKNKEDCEVEIYIKRNKDKGKNNDDACHKLAALCYTASQCPWSCSGHGECEVEIINNHTC 180
DB 121 NKKNKEDCEVEIYIKRNKDKGKNNDDACHKLAALCYTASQCPWSCSGHGECEVEIINNHTC 180
OY 181 NCDVGYGPOCQVIOCEPLLEAPBELGTMDCTHPFGNFSFSOCAPSCSEGTNLGIEETT 240
DB 181 NCDVGYGPOCQVIOCEPLLEAPBELGTMDCTHPFGNFSFSOCAPSCSEGTNLGIEETT 240
OY 241 CGPFGNWSSEPTTCOVIOCEPLSAPDLGIMNCSHPLASFSFSACFTFCSEGTNLGKRR 300
DB 241 CGPFGNWSSEPTTCOVIOCEPLSAPDLGIMNCSHPLASFSFSACFTFCSEGTNLGKRR 300
OY 301 TICSSGIMSNPSPIQCKLDRSFSMIKBDYDPLFIPVAVMTAFSGLAFTIWLARLKK 360
DB 301 TICSSGIMSNPSPIQCKLDRSFSMIKBDYDPLFIPVAVMTAFSGLAFTIWLARLKK 360
OY 361 GKSKRSMDPY 372
DB 361 GKSKRSMDPY 372
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RESULT 6
LEML_BOVIN
ID LEML_BOVIN STANDARD: PRT: 370 AA.
AC P98131:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
GN SEL.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovidae; Bos.
OC [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92164727; PubMed=1371468;
RA Walcheck B., White M., Kurk S., Kishimoto T.K., Jutila M.A.;
RT "Characterization of the bovine peripheral lymph node homing receptor: a lectin cell adhesion molecule (LECAM).";
RL Eur. J. Immunol. 22:469-476(1992).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=94055053; PubMed=7694420;
RA Bosworth B.T., Dombenke D., Shuster D.E., Harp J.A.;
RT "Bovine L-selectin: a peripheral lymphocyte homing receptor.";
RL Vet. Immunol. Immunopathol. 37:201-215(1993).
CC -1- FUNCTION: CELL SURFACE ADHESION PROTEIN. MEDIATES THE ADHERENCE OF LYMPHOCYTES TO ENDOTHELIAL CELLS OF HIGH ENDOTHELIAL VENULES IN PERIPHERAL LYMPH NODES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
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CC -----
DR EMBL: X62882; CAA44676.1;
DR HSSP: P14151; IKTJ.
DR INTERPRO: IPR000436;
DR INTERPRO: IPR000561;
DR INTERPRO: IPR001304;
DR INTERPRO: IPR002396;
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; lectin.C.1.
DR PFAM: PF00084; sushi.2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS00641; C-TYPE LECTIN_2; 1.
KW Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selection; Signal; Sushi; Repeat.
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 370
FT DOMAIN 39 333
FT TRANSMEM 334 354
FT DOMAIN 355 370
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT REPEAT 196 255
FT REPEAT 258 317
FT DISULFID 57 155
BY SIMILARITY.

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FT DISULFID 128 147 BY SIMILARITY.
FT DISULFID 160 171 BY SIMILARITY.
FT DISULFID 165 180 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 197 241 BY SIMILARITY.
FT DISULFID 227 254 BY SIMILARITY.
FT DISULFID 259 303 BY SIMILARITY.
FT DISULFID 289 316 BY SIMILARITY.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 370 AA; 41971 MW; 92168F8116A89228 CRC64;

Query Match 79.5%; Score 1682; DB 1; Length 370;
Best Local Similarity 77.0%; Pred. No. 3.2e-126;
Matches 282; Conservative 42; Mismatches 40; Indels 2; Gaps 1;

QY 1 MIFPKCSTORDIMNIRKMGWIMLCDDPLAHNGTCWTYHSEKPMNQRARFCRDN 60
DB 1 MCFPKCQNAORGLMNVFKLWIMLCDDFAHNGTCWTYHSEKPMNQRARFCRDN 60
QY 61 YTDLVAIONKAEIYELKTLTFFSRSYWIGIRKIGITWVGWTKSLTEBAEWGSGEEN 120
DB 61 YTDLVAIONKAEIYELKTLTFFSRSYWIGIRKIGITWVGWTKSLTEBAEWGSGEEN 120
QY 121 NKKKKECCVEIYIRKNDACKNDADCHIKALKALCYTASQPMSCSGHECEYIINHTC 180
DB 121 NKKKKECCVEIYIRKNDACKNDADCHIKALKALCYTASQPMSCSGHECEYIINHTC 180
QY 121 NKKKKECCVEIYIRKNDACKNDADCHIKALKALCYTASQPMSCSGHECEYIINHTC 180
DB 121 NKKKKECCVEIYIRKNDACKNDADCHIKALKALCYTASQPMSCSGHECEYIINHTC 180
QY 181 NCDVGYGPOCALYTOCEPLEAPELGTMOCTHPFGNPFSSOCAPFSGSTNLTGEFT 240
DB 181 NCDVGYGPOCALYTOCEPLEAPELGTMOCTHPFGNPFSSOCAPFSGSTNLTGEFT 240
QY 241 CGPFGNMSSEPTCOYTOCEPLASPDGLIMNCSSHPASPSFTSACTFTSESTELIGKK 300
DB 241 CGPFGNMSSEPTCOYTOCEPLASPDGLIMNCSSHPASPSFTSACTFTSESTELIGKK 300
QY 301 TIGSSGIMNPNPICOIKDKDSFMKEGDYNPFIPIVAVMTAASGLAFITWLRRLK 360
DB 301 TIGSSGIMNPNPICOIKDKDSFMKEGDYNPFIPIVAVMTAASGLAFITWLRRLK 360
QY 361 GKRSKR 366
DB 361 GKRSKR 366
QY 360 -RKSRR 364
DB 360 -RKSRR 364

RESULT 7
LEML_RAT
ID LEML_RAT STANDARD: PRT: 372 AA.
AC P30836:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE L-SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE-1) (LAM-1) (LY-22) (LYMPHOCYTE SURFACE MEL-14 ANTIGEN) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L).
GN SEL. OR LYMR OR LY-22.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92329548; PubMed=1378303;
RA Watanabe T., Song Y., Hirayama Y., Tamatani T., Kuida K., Miyasaka M.;
RT "Sequence and expression of a rat cDNA for LECAM-1.";
RL Biochim. Biophys. Acta 1131:321-324(1992).

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CC -!- SIMILARITY: CONTAINS 2 SUSHI (SCR) REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X14772; CA32880.1; -
DR EMBL: M36005; AAA39722.1; -
DR EMBL: M36058; AAA39723.1; -
DR EMBL: M25324; -; NOT_ANNOTATED_CDS.
DR EMBL: M64549; AAA75651.1; -
DR EMBL: M64440; AAA75651.1; JOINED.
DR EMBL: M64545; AAA75651.1; JOINED.
DR EMBL: M64548; AAA75651.1; JOINED.
DR PIR: A32375; A32375.
DR HSSP: P14151; IKUH.
DR MGD: MGI:96279; SELL.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002386; -.
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; Lectin_c; 1.
DR PFAM: PF00084; sush1; 2.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sush1; Repeat.
KM
FT SIGNAL 1 28
FT PROPEP 29 38
FT CHAIN 39 372
FT DOMAIN 39 332
FT TRANSMEM 333 355
FT DOMAIN 356 372
FT DOMAIN 55 155
FT DOMAIN 156 192
FT DOMAIN 196 317
FT REPEAT 196 255
FT REPEAT 258 317
FT DISULFID 57 135
FT DISULFID 128 147
FT DISULFID 160 171
FT DISULFID 165 180
FT DISULFID 182 191
FT DISULFID 197 241
FT DISULFID 227 254
FT DISULFID 259 303
FT DISULFID 289 316
FT CARBOHYD 60 104
FT CARBOHYD 104 177
FT CARBOHYD 177 216
FT CARBOHYD 216 226
FT CARBOHYD 226 246
FT CARBOHYD 246 278
FT CARBOHYD 278 288
FT CARBOHYD 288 308
FT CARBOHYD 308 320
FT CONFLICT 32 32
FT SEQUENCE 372 AA; 42288 MM; 4433EDPEACB2B78 CRC64;

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Query Match 78.0%; Score 1651; DB 1; Length 372;  
 Best Local Similarity 76.1%; Pred. No. 9, 1e-124;  
 Matches 283; Conservative 32; Mismatches 57; Indels 0; Gaps 0;

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QY 1 MIFPMKCGSTORDLNIIFKMGCTMCCDFLAHGTGCTWYHSEKPMNMORARFCRDN 60
   1:||||:| 11 ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MIFPMKCGSTGYWSRNITLMTWTLCCDFLIHGHGTHCMTHYSEKPMNMENARFKCN 60
   1:||||:| 11 ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 YNDLVAIONKAELEYLEKTLFPSRSYWMIGTRKIGITWGTNKSLEENENNGDSEPN 120
   61 YNDLVAIONKRELEYLENTLPSRYWIGTRKIGKMTWGTNKTTRKEAENNGAGEPN 120
QY 121 NKKNEDEVEIYIKRNKDGAKNNDACRKLKAALCYTASCPMWSGSGHECVETINNHTC 180
   121 NKKNEDEVEIYIKRERDSGKNNDACRKLKAALCYTASCPMWSGSGHECVETINNHTC 180
QY 181 NDDVGYVGPQCVLTQCPLPAPELGTMDCTHPGNGFSFSCAFSGSEGTNLGLEETP 240
   181 IDDAVGYGPQCVYQCBLEPAPELGTMDCTHPGNGFSFSCAFSGSEGTNLGLEETP 240
QY 241 GPFENMSSPEPTCOVICPELSPADGIMNCSPHPLASFSTACTCTGCEGELLGKK 300
   241 CGASGNMSSPEPTCOVICPELSPADGIMNCSPHPLASFSTACTCTGCEGELLGTA 300
Db 241 CGASGNMSSPEPTCOVICPELSPADGIMNCSPHPLASFSTACTCTGCEGELLGTA 300
QY 301 TICSSGIWNSPPIQKLDKFSMIKEGDYNPFIPEAVWTAFSGLAFIIMLARRLK 360
   301 TICGASGNMSSPEPTCOVETNRFSKIREGDYNPFIPEAVWTAFSGLAFIIMLARRLK 360
QY 361 GKSKRSNNDPY 372
   361 GKSKRSNNDPY 372
Db 361 GKSKRSNNDPY 372

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RESULT 9
LEM3_SHEEP STANDARD; PRT; 769 AA.
ID LEM3_SHEEP
AC P98109;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (PADGEM)
DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP.
OS Ovis aries (Sheep).
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RL Burns S.A., Neufeld E.J., Donady J.J.;
   Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -!- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
CC -!- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L34270; AAB59261.1; -
DR HSSP: P16109; IFSB.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002386; -.
DR PFAM: PF00008; EGF_1.

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Db	65	TDLVAIQKNEIAYLNETIPIYNSYWMIGIKIDNKMWTGKTKTLLEAEENMADNEPNN	12
Qy	122	KKNKEDVEYIYIKRNKADGAKKNDADACHLKAALCYTASQPMSCSGHGVEYIINHTCN	181
Db	125	KKNNDQCEYIETIKSPASPAKWNNDPCKRKALCYRASQPMSCSKQCEIETIGNTCS	184
Qy	182	CDVGVGGQOOLVIOCEPLEPELGTMDCTHPGNFSGSCAFSCSGEINLGIETTC	241
Db	185	CYPGVGEGCEYVEGCEFDLPQVHNHMSCHPLDNFSGSCSHCAEGYALNPRELC	244
Qy	242	GPFGNMSSPEPTCCVIOICEPLSADLIGMNSHPLASFEFTSACTFYCSGGTELIGKKT	301
Db	245	LASGIWNSPPQCAVACCPALKSPEGSGMSCFHAKAFQHDSSCSFGCEGFTLVGEVY	304
Qy	302	ICESSGIWSNPSPIQKL 319	
Db	305	HCTALGVWTAPTPVCKAI 322	
RESULT	10		
LEM3	HUMAN	STANDARD;	PRT; 830 AA.
AC	PI6109;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-AUG-1990 (Rel. 15, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM		
DE	(CD62) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).		
GN	SELP OR GMP.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=89168432; PubMed=246574;		
RA	Johnston G.T., Cook R.G., McEver R.P.;		
RT	"Cloning of GMP-140, a granule membrane protein of platelets and		
RT	endothelium: sequence similarity to proteins involved in cell		
RT	adhesion and inflammation.";		
RL	Cell 56:1033-1044(1989).		
RN	[2]		
RP	PALMITOYLATION.		
RX	MEDLINE=9326559; PubMed=7684381;		
RA	Fujimoto T., Stroud E., Whalley R.E., Prescott S.M., Muszbek L.,		
RA	Laposata M., McEver R.P.;		
RT	"P-selectin is acylated with palmitic acid and stearic acid at		
RT	cysteine 766 through a thioester linkage.";		
RL	J. Biol. Chem. 268:11394-11400(1993).		
RN	[3]		
RP	STRUCTURE BY NMR OF 160-199.		
RX	MEDLINE=97057176; PubMed=8901515;		
RA	Freeman S.J., Sanford D.G., Bachovchin W.W., Furie B.C., Baluja J.D.,		
RA	Furie B.;		
RT	"Structure and function of the epidermal growth factor domain of P-		
RT	selectin.";		
RL	Biochemistry 35:13733-13744(1996).		
RN	[4]		
RP	3D-STRUCTURE MODELING OF 42-161.		
RX	MEDLINE=94093388; PubMed=7505680;		
RA	Bajorath J., Stenckamp R., Aruffo A.;		
RT	"Knowledge-based model building of proteins: concepts and examples.";		

RP: VARIANT: ASN-331; ASP-603; VAL-640 AND PRO-756.  
RX: MEDLINE:98334547; PubMed-96661170;  
RA: Hermann S.M., Ricard S., Nicaud V., Mallet C., Evans A.,  
RA: Ridgwaets J.B., Arveiller D., Luc G., Cambien F.;  
RT: "The P-selectin gene is highly polymorphic: reduced frequency of the  
RT: p7075 allele carriers in patients with myocardial infarction.";  
RL: Hum. Mol. Genet. 7:1277-1284(1998).  
CC: -I- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS  
CC: TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE  
CC: INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH

DR	EMBL:	M60234;	AAA35910.1;	-;
DR	EMBL:	M60217;	AAA35910.1;	JOINED.
DR	EMBL:	M60218;	AAA35910.1;	JOINED.
DR	EMBL:	M60219;	AAA35910.1;	JOINED.
DR	EMBL:	M60224;	AAA35910.1;	JOINED.
DR	EMBL:	M60223;	AAA35910.1;	JOINED.
DR	EMBL:	M60224;	AAA35910.1;	JOINED.
DR	EMBL:	M60225;	AAA35910.1;	JOINED.
DR	EMBL:	M60226;	AAA35910.1;	JOINED.
DR	EMBL:	M60227;	AAA35910.1;	JOINED.
DR	EMBL:	M60228;	AAA35910.1;	JOINED.
DR	EMBL:	M60229;	AAA35910.1;	JOINED.
DR	EMBL:	M60231;	AAA35910.1;	JOINED.
DR	EMBL:	M60232;	AAA35910.1;	JOINED.
DR	EMBL:	M60233;	AAA35910.1;	JOINED.
DR	EMBL:	M25322;	-;	NOT_ANNOTATED_CDS.
DR	PIR:	A30359;	A30359.	
DR	PDB:	1FSB;	01-APR-97.	
DR	PDB:	IKD;	03-APR-96.	
DR	MTM:	I73610;	-;	
DR	INTERPRO:	IPR000436;	-;	
DR	INTERPRO:	IPR000561;	-;	
DR	INTERPRO:	IPR001304;	-;	
DR	INTERPRO:	IPR002396;	-;	
DR	PFAM:	PF00008;	EGF_1.	
DR	PFAM:	PF00059;	Lectin-C; 1.	
DR	PFAM:	PF00084;	sushi; 9.	
DR	PRINTS:	PR00343;	SELECTIN.	
DR	PROSITE:	PS00022;	EGF_1; 1.	
DR	PROSITE:	PS01186;	EGF_2; 1.	
DR	PROSITE:	PS00615;	C-TYPE_LECTIN_1; 1.	
DR	PROSITE:	PS00041;	C-TYPE_LECTIN_2; 1.	
KW	Cell adhesion;	Transmembrane;	Glycoprotein;	EGF-like domain; Lectin;
KW	Selectin; Signal;	Sushi;	Repeat;	Lipoprotein; Palmitate; Polymorphism;
KW	3D-structure.			
FT	SIGNAL	1	41	
FT	CHAIN	42	830	P-SELECTIN.
FT	DOMAIN	42	771	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	772	795	POTENTIAL.
FT	DOMAIN	796	830	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	58	158	C-TYPE LECTIN (SHORT FORM).
FT	DOMAIN	159	195	
FT	REPEAT	199	762	9 X SUSHI (SCR) REPEATS.
FT	REPEAT	199	258	
FT	REPEAT	261	320	SUSHI 1.
FT	REPEAT	323	382	SUSHI 2.
FT	REPEAT	385	444	SUSHI 3.
FT	REPEAT	447	506	SUSHI 4.
FT	REPEAT	509	568	SUSHI 5.
FT	REPEAT	571	630	SUSHI 6.
FT	REPEAT	641	700	SUSHI 7.
FT	REPEAT	703	762	SUSHI 8.
FT	REPEAT			SUSHI 9.

Query Match	Best Local Similarity	Matches 157; Conservative 157; Mismatches 106; Indels 0; Gaps 0;
QY 8 OSTQDLMNIRKLMGWTMLCCDFLAHHGTYCWTYHYSERKPNMOWARPCRDYVTDLVAI 67	42.8%; Score 905; DB 1; Length 830;	
Db 11 ORFOGVVFGISQLCFESALITLNOKEVAAMTYSTKAYSMNISKYQONRYTDLVAI 70	50.6%; Pred. No. 2.6e-64;	
QY 68 ONKEIEYLEKTPFSKSYWIGIRKIGITWWTGNTSLTEELZEMNGDEDPNNKKNKED 127		
Db 71 ONKNEIDYLNKVIIPYSSYYWIGIRKNNKTWTWGTGKALTNENAEADNEPNKKNBNED 130		
QY 128 CVELYIKRNNDACKNNDKCHKIKALCYTASCPWSCGSHCEVELIINHTNCNDVGY 187		
Db 131 CVELYIKSPAPKRWDEHCLKKHALCYTASCDMSCKSGKGELEITIGNYTCSCIPGY 190		
QY 188 GPQCOLVIOCEPLELEAFELCTMDCTHPFNFSFSSOCAFSSSEGNLTGLETTCCPGNW 247		
Db 191 GPCECVYREGCELELPQHVILMNCSPRLCNEFFNSQCSFHCCTGYVNGPSKLECLASGIW 250		
QY 248 SSPEPTQVYIQCEPPLSADPLGIMNCSHPLASFSYTSACTPGCEGTELLGKKKTCSSG 307		
Db 251 TNNPQCLAAQCCPLKTPRGNMICILSHAKKAFQHQSSCSFSCGEGALVATGPWVQNTTCG 310		



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07 308 1WSNRPIC0 317
Db 311 WTAAPAVCK 320

RESULT 11
LEMS_MOUSE STANDARD: PRT: 768 AA.
ID LEMS_MOUSE Q01102:
AC 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM
DE (CD62P) (LEUCOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
DE SELP OR GMP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN 11)
RP SEQUENCE FROM N.A.
RX MEDLINE=92340571; PubMed=1378846;
RA Weller A., Isenmann S., Vestweber D.;
RT "Cloning of the mouse endothelial selectins. Expression of both E-
RT and p-selectin is inducible by tumor necrosis factor alpha.";
RL J. Biol. Chem. 267:15176-15183(1992).
RN 12)
RP SEQUENCE FROM N.A.
RX MEDLINE=92345617; PubMed=1379089;
RA Sanders W.E. Jr., Wilson R.W., Ballantyne C.M., Beaudet A.L.;
RT "Molecular cloning and analysis of in vivo expression of murine P-
RT selectin.";
RL Blood 80:795-800(1992).
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
CC AND WEIBEL-PLADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
CC ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
CC THE CELL SURFACE.
CC -1- INDUCTION: BY TUMOR NECROSIS FACTOR ALPHA.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS. MOUSE P-LECTIN LACKS
CC THE HUMAN SUSHI-2 EQUIVALENT.
CC
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CC -----
DR EMBL: M87861; AAA40008.1; -
DR EMBL: M72332; AAA37712.1; -
DR PIR: A42755; A42755.
DR HSSP: P16109; IFSB.
DR MGD: MGI:98280; SELP.
DR INTERPRO: IPR000436; -
DR INTERPRO: IPR000561; -
DR INTERPRO: IPR001304; -
DR INTERPRO: IPR002396; -
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; LECTIN_C; 1.
DR PFAM: PF00084; SUSHI_8.
DR PRINTS: PR00343; LECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.

```

[illegible]

```

RESULT 12
LEM3_BOVIN STANDARD; PRT; 646 AA.
ID LEM3_BOVIN
AC P42201;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eultheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-CAPILLARY ENDOTHELIUM;
RX MEDLINE-93249394; PubMed-7683458;
RA Strubel N.A., Nguyen M., Kansas G.S., Tedder T.F., Bischoff J.;
RT "Isolation and characterization of a bovine cDNA encoding a
RL functional homolog of human P-selectin."
CC Biochem. Biophys. Res. Commun. 192:338-344(1993).
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
CC AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
CC ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
CC THE CELL SURFACE.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC THE HUMAN SUSHI-3, -4 AND -7 EQUIVALENTS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L12041; AAA30743.1; -.
DR HSSP: P16109; IFSB.
DR INTERPRO: IPR000436; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001304; -.
DR INTERPRO: IPR002396; -.
DR PFAM: PF00008; EGF_1.
DR PFAM: PF00059; lectin_c; 1.
DR PFAM: PF00084; sushi; 6.
DR PRINTS: PR00343; SELECTIN.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_2; 1.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; lectin;
KW Selectin; Signal; Sushi; Repeat.
FT SIGNAL 1 41
FT CHAIN 42 646
FT DOMAIN 42 587
FT TRANSMEM 588 611
FT DOMAIN 612 646
FT DOMAIN 58 158
FT DOMAIN 159 195
FT DOMAIN 199 258
FT REPEAT 199 258
FT REPEAT 261 320
SUSHI 1.
SUSHI 2.

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FT REPEAT 323 382
FT REPEAT 385 444
FT REPEAT 457 516
FT REPEAT 519 578
FT DISULFD 131 158
FT DISULFD 163 174
FT DISULFD 168 183
FT DISULFD 185 194
FT DISULFD 200 244
FT DISULFD 230 257
FT DISULFD 262 306
FT DISULFD 292 319
FT DISULFD 324 368
FT DISULFD 354 381
FT DISULFD 386 430
FT DISULFD 416 443
FT DISULFD 458 502
FT DISULFD 488 515
FT DISULFD 520 564
FT DISULFD 550 577
FT CARBOHYD 48 54
FT CARBOHYD 54 54
FT CARBOHYD 80 80
FT CARBOHYD 180 180
FT CARBOHYD 212 212
FT CARBOHYD 219 219
FT CARBOHYD 336 336
FT CARBOHYD 481 481
FT CARBOHYD 532 532
FT CARBOHYD 539 539
FT CARBOHYD 557 557
FT SITE 634 637
SO SEQUENCE 646 AA; 71229 MW; 57391244627A6ACA CRC64;

```

Query Match 42.3%; Score 894.5; DB 1; Length 646;  
 Best local Similarity 48.7%; Pred. No. 1,3e-63;  
 Matches 155; Conservative 51; Mismatches 109; Indels 3; Gaps 1;

```

QY 2 IFPWKQSTQRODLMNFKLMGWTMLCCDFLAHNGTYCWTYHSEKPNMQARRCRDNY 61
   8 IIMWR--PQRAVERIVOLLCSVLFEVINQKEVSAMTYHSMKTYSMYSRAPFCQKY 64
DB TDVAIONKNEIAYLNETIPYNSIYWGIRKINKMTWGTGKTLTEEDENMADNEPNN 124
QY 122 KKKEDCVEIYIKRNKDKAMNDACHRLKAALCYTASCQPMSCSGHQECVEIINHTCN 181
   125 KRNDQCVETIYIKSLASGKMNDEPCWKRKRALCYRASQPMSCSKQEGCIETIGNTCS 184
QY 182 CDVGYGPGCCOLVIOCEPLEAPDELGTMDCTHPFGNFSFSSQCAFSGEGTNLGIETTC 241
   185 CYGFGTGPCEYVREGCEFDLPQHYNMCSHPLGNFNSHSCSFHCAEGYALNPSFLC 244
QY 242 GPGNWSPEPTQYIOCEPLSAPDLGIMNCSHPLASFSFSACTGICSTGLIGAKKT 301
   245 IASGIMTNSPPQCVAVGCPALKSPGSGMSCVQSAEAFQHOSSCSFSCEGFALVGEVY 304
QY 302 ICESGIMNSNPICQKL 319
DB 305 HCTALGVMTAPVCKAL 322

```

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RESULT 13
LEM3_RAT STANDARD; PRT; 768 AA.
ID LEM3_RAT
AC P96106;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)

```

DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).  
 GN SELP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG;  
 RX MEDLINE=9433817; PubMed=7520013;  
 RA Auchampach J.A., Oliver M.G., Anderson D.C., Manning A.M.;  
 RT "Cloning, sequence comparison and in vivo expression of the gene  
 RL encoding rat p-selectin".  
 CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS  
 TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE  
 INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH  
 LEUKOCYTES. THE LIGAND RECOGNIZED IS STALTY-LEWIS X.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,  
 CC LUNG, BRAIN, LIVER, HEART, KIDNEY, THYMUS, SMALL INTESTINE.  
 CC -1- INDUCTION: ACUTE INFLAMMATION (PROBABLY).  
 CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; RAT P-LECTIN LACKS THE  
 HUMAN SUSHI-2 EQUIVALENT.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; L23088; AAA60325.1; -.  
 DR HSSP; P16109; IFSB.  
 DR INTERPRO: IPRO00436; -.  
 DR INTERPRO: IPRO00561; -.  
 DR INTERPRO: IPRO01304; -.  
 DR INTERPRO: IPRO02396; -.  
 DR PFAM: PF00059; lectin\_c; 1.  
 DR PFAM: PF00084; sush1; 8.  
 DR PRINTS: PRO0343; SELECTIN.  
 DR PROSITE: PS00022; EGF\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 1.  
 DR PROSITE: PS00615; C-TYPE\_LLECTIN\_1; 1.  
 DR PROSITE: PS50041; C-TYPE\_LLECTIN\_2; 1.  
 KM Cell adhesion: Transmembrane; Glycoprotein; EGF-like domain; Lectin;  
 Selectin; Signal; Sush1; Repeat; Lipoprotein; Palmitate.  
 FT SIGNAL 1 41  
 FT CHAIN 42 768  
 FT DOMAIN 42 709  
 FT TRANSMEM 710 733  
 FT DOMAIN 734 768  
 FT DOMAIN 58 158  
 FT DOMAIN 159 195  
 FT DOMAIN 199 258  
 FT REPEAT 199 258  
 FT REPEAT 261 320  
 FT REPEAT 323 382  
 FT REPEAT 385 444  
 FT REPEAT 447 506  
 FT REPEAT 509 568  
 FT REPEAT 579 638  
 FT REPEAT 641 700  
 FT DISULEID 60 158  
 FT DISULEID 131 150  
 FT DISULEID 168 183  
 FT DISULEID 185 194  
 FT DISULEID 200 244  
 FT DISULEID 230 257  
 FT DISULEID 262 306

FT DISULEID 292 319 BY SIMILARITY.  
 FT DISULEID 324 368 BY SIMILARITY.  
 FT DISULEID 354 381 BY SIMILARITY.  
 FT DISULEID 386 430 BY SIMILARITY.  
 FT DISULEID 416 443 BY SIMILARITY.  
 FT DISULEID 448 492 BY SIMILARITY.  
 FT DISULEID 478 505 BY SIMILARITY.  
 FT DISULEID 510 554 BY SIMILARITY.  
 FT DISULEID 540 567 BY SIMILARITY.  
 FT DISULEID 580 624 BY SIMILARITY.  
 FT DISULEID 610 637 BY SIMILARITY.  
 FT DISULEID 642 686 BY SIMILARITY.  
 FT DISULEID 672 699 BY SIMILARITY.  
 FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 212 212 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 654 654 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 661 661 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT LIPID 745 745 PALMITATE (BY SIMILARITY).  
 FT SITE 756 759 ENDOCYTOSIS SIGNAL (PROBABLE).  
 SQ SEQUENCE 768 AA; 83517 MW; 26FD78A5F3E1316 CRC64;  
 Query Match 41.8%; Score 885; DB 1; length 768;  
 Best Local Similarity 53.4%; Pred. No. 9e-63;  
 Matches 150; Conservative 42; Mismatches 89; Indels 0; Gaps 0;  
 QY 39 WYHNSKRRPMWQRRARRCRONTYDVALQKAELEYLEKTLPSRSYVYIGIRIGGIW 98  
 DB 42 WYNYSTKAYSMNNSRAKCRHFTDLVALQNKNEIHLANDYIPVANSYWGIRINKWK 101  
 QY 99 TWGCTNKSLETEAEENWGDGEPNNKKNKEDCEIYIKRRKDGKWNDDACIHLKALCYTA 158  
 DB 102 TWGCTNKTTLAEENWADNEPNNKRNNDCEIYIKKSASAGKWNDECFKRRKALCYTA 161  
 QY 159 SCQPMWCSGHEGCEYIINNHTCNCDDVGYGPGCOLVIOCEPLAEPLCTMDCTHPFGNFS 218  
 DB 162 SCQPMWCSGHEGCEYIINNHTCNCDDVGYGPGCOLVIOCEPLAEPLCTMDCTHPFGNFS 221  
 QY 219 FSSQCAFSCSGSTNLTGIEFTTCGFGWSSPEPICOVIOCEPLASAPDLGTMNSHPLAS 278  
 DB 222 FSSQCAFSCSGSTNLTGIEFTTCGFGWSSPEPICOVIOCEPLASAPDLGTMNSHPLAS 281  
 QY 279 FSTFSACFFICSEGTGELIGKRRKKTICSESSGIMSNPSPTQRL 319  
 DB 282 FAYDSSCKFECPGTRMRGSDILHCTDSGOWSEPLPTCEAI 322  
 RESULT 14  
 ID LEM2\_HUMAN STANDARD; PRT: 610 AA.  
 AC P16581; P16111;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-AUG-1990 (Rel. 15, last sequence update)  
 DT 15-JUL-1999 (Rel. 38, last annotation update)  
 DE E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)  
 DE (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)  
 DE (CD62E).  
 GN SELE OR ELAM1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90175359; PubMed=1689848;  
 RA Hession C., Osborn L., Goff D., Chi-Rosso G., Vassallo C.,  
 RA Paasek M., Plitack C., Tizard R., Goetz S., McCarthy K., Hopple S.,  
 Lobb R.;







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OM protein - protein search, using sw model

Run on: January 13, 2001, 01:14:23 ; Search time 77.13 seconds  
(without alignments)  
565.297 Million cell updates/sec

Title: US-09-119-209-2  
Perfect score: 2116  
Sequence: 1 MIFPMKOSTORDLWNIKFL.....MLARRLKGGKKSRMNDPY 372

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP.REFML\_15:\*  
2: SP.Archea:\*  
3: SP.Bacteria:\*  
4: SP.fungi:\*  
5: SP\_human:\*  
6: SP\_invertebrate:\*  
7: SP\_mhc:\*  
8: SP.organelle:\*  
9: SP.phage:\*  
10: SP\_plant:\*  
11: SP\_rodent:\*  
12: SP\_virus:\*  
13: SP\_vertebrate:\*  
14: SP\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2090	98.8	385	4 Q9UJ43	Q9UJ43 homo sapien
2	1796	84.9	376	6 Q28629	Q28629 oryctolagus
3	1667	78.8	372	11 Q63762	Q63762 ratulus norv
4	911	43.1	616	4 Q95509	Q95509 homo sapien
5	909	43.0	740	4 Q95507	Q95507 homo sapien
6	898	42.4	740	4 Q95508	Q95508 homo sapien
7	884	41.8	754	6 Q28290	Q28290 canis famli
8	876.5	41.4	646	6 Q29097	Q29097 sus scrofa
9	860.5	40.7	649	6 Q28657	Q28657 oryctolagus
10	815.5	38.5	482	6 Q28982	Q28982 sus scrofa
11	247.5	11.7	1124	5 Q9VYR4	Q9VYR4 drosophila
12	237.5	11.2	974	5 P91658	P91658 drosophila
13	236	11.2	868	5 Q18849	Q18849 caenorhabdi
14	216	10.2	1061	5 Q9VXX7	Q9VXX7 drosophila
15	199.5	9.4	449	4 Q14570	Q14570 homo sapien
16	199.5	9.4	449	4 Q9NU86	Q9NU86 homo sapien
17	199.5	9.4	1172	4 Q9NU87	Q9NU87 homo sapien
18	195	9.2	958	5 Q9V560	Q9V560 drosophila
19	189.5	9.0	1083	5 Q26423	Q26423 carcinoscor

20	183	8.6	328	4 Q9UJ71	Q9UJ71 homo sapien
21	176	8.3	378	6 Q62837	Q62837 saguinus oe
22	175.5	8.3	2014	6 Q29530	Q29530 pan troglod
23	174.5	8.2	1652	5 Q9VU9	Q9VU9 drosophila
24	172	8.1	2039	4 Q16745	Q16745 homo sapien
25	172	8.1	2489	4 Q16744	Q16744 homo sapien
26	171.5	8.1	395	12 Q9J2M6	Q9J2M6 macaca mula
27	171	8.1	354	5 Q9U611	Q9U611 drosophila
28	171	8.1	359	5 Q9V0X3	Q9V0X3 drosophila
29	170	8.0	314	6 Q62835	Q62835 saguinus oe
30	170	8.0	404	4 Q9NMX6	Q9NMX6 homo sapien
31	169.5	8.0	559	4 Q9UQV2	Q9UQV2 homo sapien
32	168	7.9	292	4 Q14538	Q14538 homo sapien
33	168	7.9	533	11 Q08569	Q08569 cavia porce
34	166	7.8	1911	6 Q29528	Q29528 papio hamad
35	165.5	7.8	560	5 Q22328	Q22328 caenorhabdi
36	165.5	7.8	1479	11 Q64449	Q64449 mus musculu
37	165	7.8	287	4 Q03969	Q03969 homo sapien
38	165	7.8	292	4 Q00448	Q00448 homo sapien
39	164.5	7.8	377	6 Q62838	Q62838 saguinus oe
40	164	7.8	214	11 Q9R008	Q9R008 mus musculu
41	164	7.8	339	11 P97261	P97261 cavia porce
42	164	7.8	661	6 Q29531	Q29531 pan troglod
43	163	7.7	269	5 Q24696	Q24696 dugesia tlig
44	163	7.7	669	6 Q28085	Q28085 bos taurus
45	162.5	7.7	379	11 P70105	P70105 cavia porce

## ALIGNMENTS

RESULT 1  
ID Q9UJ43 PRELIMINARY: PRT: 385 AA.  
AC Q9UJ43:  
DT 01-MAY-2000 (TRENBLREL. 13, Created)  
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)  
DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)  
DE L-SELECTIN PRECURSOR.  
GN L-SELECTIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-HEMATOPOIETIC (B LYMPHOCYTE);  
RA Flegler C.B.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-HEMATOPOIETIC (B LYMPHOCYTE);  
RA Flegler C.B.;  
RL Thesis (1998), Freie Universitaet Berlin, Fachbereich Chemie.  
DR HSSP: P14151; IKB.  
DR INTERPRO: IPR000436; -  
DR INTERPRO: IPR000561; -  
DR INTERPRO: IPR001304; -  
DR INTERPRO: IPR002396; -  
DR PFAM: PF00008; EGF\_1.  
DR PFAM: PF00059; Lectin\_C\_1.  
DR PFAM: PF00084; sushi\_2.  
DR PRINTS: PR00343; SELECTIN.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS00615; C-TYPE LECTIN\_1; 1.  
DR PROSITE: PS01186; EGF\_2; 1.  
DR PROSITE: PS50041; C-TYPE LECTIN\_2; 1.  
KW Signal; Lectin; Selectin.  
FT SIGNAL 52 385 POTENTIAL.  
FT CHAIN 1 51 L-SELECTIN.  
SQ SEQUENCE 385 AA; 43617 MW; 1205F691BA638EF1 CRC64;

Matches	368;	Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0;
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RESULT	2			
028629				
ID	028629	PRELIMINARY;	PRT;	376 AA.
AC	028629			
DT	01-NOV-1996 (Tremblrel_01, Created)			
DT	01-NOV-1996 (Tremblrel_01, Last sequence update)			
DT	01-MAY-2000 (Tremblrel_13, Last annotation update)			
DE	l-SELECTIN PRECURSOR.			
OS	Oryctolagus cuniculus (Rabbit).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eultheria; Lagomorpha; Leporidae; Oryctolagus.			
OX	NCBI_TaxID=9986;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=KIDNEY, CORTEX;			
RA	Qian J., Marks R.M.;			
RL	Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: U26535; AAA67896.1; -.			
DR	HSSP: P14151; 1k1B.			
DR	INTERPRO: IPR000436; -.			
DR	INTERPRO: IPR000561; -.			
DR	INTERPRO: IPR001304; -.			
DR	INTERPRO: IPR002396; -.			
DR	PFAM: PF00008; EGF_1.			
DR	PFAM: PF00059; Lectin_C_1.			
DR	PFAM: PF00084; sushi_2.			
DR	PRINTS: PR00343; SELECTIN.			
DR	PROSITE: PS00022; EGF_1; UNKNOWN_1.			
DR	PROSITE: PS00615; C_Type_Lectin_1; 1.			
DR	PROSITE: PS01186; EGF_2; 1.			
DR	PROSITE: PS50041; C_Type_Lectin_2; 1.			
KM	Signal; Lectin; Glycoprotein.			
FT	SIGNAL			
FT	CHAIN	1	39	POTENTIAL.
FT	CHAIN	39	376	l-SELECTIN.
SQ	SEQUENCE	376 AA;	42336 MW;	59FE6D530F490947 CRC64;

Query Match	84.9%;	Score 1796;	DB 6;	Length 376;
Best Local Similarity	84.1%;	Pred. No. 5.1e-168;		

1 MIEPWKCQSTQRDWNIFKLGWMTLCCDFLAHHGYCWTYHYSEKPMNQARARFCRDN 60

RESULT	3	
ID	063762	PRELIMINARY;
NO	063762	PRT;
		372 AA

DT 01-NOV-1996 (TREMBLREL\_01, Created)  
 DT 01-NOV-1996 (TREMBLREL\_01, Last sequence update)  
 DT 01-OCT-2000 (TREMBLREL\_15, Last annotation update)  
 DE LYMHOCTE MEMBRANE PROTEIN A.11.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN 111  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=95369821; PubMed=7543874;  
 RA Sackstein R., Meng L., Xu X.M., Chin Y.H.;  
 RT "Evidence of post-transcriptional regulation of L-selectin gene  
 RL expression in rat lymphoid cells."; Immunology 85:198-204(1995)  
 DR EMBL: S79523; MAF60710.2; -.  
 DR HSSP: P1A151; 1KJB.  
 DR INTERPRO: IPR000436; -.  
 DR INTERPRO: IPR000561; -.  
 DR INTERPRO: IPR001304; -.  
 DR INTERPRO: IPR002396; -.  
 DR PFAM: PF00008; EGF\_1.  
 DR PFAM: PF00059; lectin\_C; 1.  
 DR PFAM: PF00084; sushi; 2.  
 DR PRINTS: PRO0343; SELECTIN.  
 DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
 DR PROSITE: PS00615; C\_TYPE\_LLECTIN\_1; 1.  
 DR PROSITE: PS01186; EGF\_2; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 SQ SEQUENCE 372 AA: 42471 MW: 726125610DDDE4A CRC64;

Query Match	78.8%	Score 1667	DB 11	Length 372
Best Local Similarity	77.2%	Pred. No. 2.3e-155		
Matches 287	Conservative 35	Mismatches 150	Indels 0	Gaps 0
1 MIPWKCSTQDIDNINIFKLGWTLCCDFLAHNGTCWTVHYSEKPMNQARARFCRDN 60				



```
Db 1 MFVPRCSAGRGSWSLKLMITWLLCCDLLPHNCHTCHWTYHSRSMNWEARKECHN 60
Qy 61 YTDLVAIONKAEIEYLEKTLPEFSRSYWIIGIRKIGIWTWGTNKSLEAEANMGDGRN 120
Db 61 YTDLVAIONKAEIEYLEKTLPEFSRSYWIIGIRKIGIWTWGTNKSLEAEANMGDGRN 120
Qy 121 NKKNKEDCEVEIYIKRNKDGAKMNDACHKRLKAALCYTASCPWSCSGHGECEIINNHTC 180
Db 121 NKKNKEDCEVEIYIKRNKDGAKMNDACHKRLKAALCYTASCPWSCSGHGECEIINNHTC 180
Qy 181 NCDGYVYPCQOLVIQCEPPLAPELGTMDCTHIFGNSFSQCAFSCSEGTNLGIETT 240
Db 181 ICDGYYPCQOYVYQCEPPLAPELGTMTNCHTIFLDFSFQSCAFNCSGSELLGNATKE 240
Qy 241 CGPFGNMSPTPCOVIOCEPPLASAPDLGIMNCSHPLASFSTACTFICSEGTNLGK 300
Db 241 CGASGNMTYLEPICOVIOCMPLAPDLGTMECSHPLANSFTSACTFICSEGTDLIGERK 300
Qy 301 TICSSGIMSNPSPIQOKLDFKSFMSIKEGDYNPFLIPAVAVTAFSGLAFTIWLARLKK 360
Db 301 TVCSGSSGMSWSPICQKTRKFSKIKEGDYNPLFIPIAVAVTAFSGLAFTIWLARLKK 360
Qy 361 GKSKRSRNDPY 372
Db 361 GKSKQERMDPY 372

RESULT 4
095509 PRELIMINARY; PRT; 616 AA.
AC 095509;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE DJ780M13.1.3 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140 KDA, ANTIGEN
CD62, GMP140)) (ISOFORM 3) (FRAGMENT).
GN SELP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Howden P.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022146; CAA18144.1; -.
DR HSSP; P16109; IKJD.
DR INTERPRO; IPR000436; -.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001304; -.
DR INTERPRO; IPR002396; -.
DR PFAM; PF00008; EGF_1.
DR PFAM; PF00059; lectin_C; 1.
DR PRINTS; PR00343; SELECTIN.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
FT NON_TER 616
SQ SEQUENCE 616 AA; 67735 MW; 35CDABFAD61D724 CRC64;

Query Match 43.1%; Score 911; DB 4; Length 616;
Best Local Similarity 50.6%; Pred. No. 5.9e-81;
Matches 158; Conservative 47; Mismatches 107; Indels 0; Gaps 0;
```

```
Db 71 QNKNEIDYLNKLVPIYSSYWIIGIRKKNKTWGTWTKKALTNEAEANMDNEPNRNHED 130
Qy 128 CVEIYIKRNKDGAKMNDACHKRLKAALCYTASCPWSCSGHGECEIINNHTCNDVGY 187
Db 131 CVEIYIKRSPASGAKMNDACHKRLKAALCYTASCPWSCSGHGECEIINNHTCNDVGY 190
Qy 188 GPQCOLVIOCEPPLAPELGTMDCTHIFGNSFSQCAFSCSEGTNLGIETTGPFGNW 247
Db 191 GPECYVYECGTELPQVHVMNCSHPLGNSFSQCAFSCSEGTNLGIETTGPFGNW 250
Qy 248 SSPEPTCOVIOCEPPLAPDLGIMNCSHPLASFSTACTFICSEGTNLGKRTICSSG 307
Db 251 TNKPPQCLAAOCPPLKIPBERGNMCLHSAKAFQHQSSCSFSGEEGFAIVGPEVVOCTASG 310
Qy 308 TMSNPSPIQOKL 319
Db 311 VWTAPAPVCKAL 322

RESULT 5
095507 PRELIMINARY; PRT; 740 AA.
AC 095507;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE DJ780M13.1.1 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140 KDA, ANTIGEN
CD62, GMP140)) (ISOFORM 1) (FRAGMENT).
GN SELP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Howden P.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022146; CAA18142.1; -.
DR HSSP; P16109; IKJD.
DR INTERPRO; IPR000436; -.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001304; -.
DR INTERPRO; IPR002396; -.
DR PFAM; PF00008; EGF_1.
DR PFAM; PF00059; lectin_C; 1.
DR PRINTS; PR00343; SELECTIN.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
FT NON_TER 740
SQ SEQUENCE 740 AA; 81095 MW; 3B5F70A45B1A3CD4 CRC64;

Query Match 43.0%; Score 909; DB 4; Length 740;
Best Local Similarity 50.3%; Pred. No. 1.1e-80;
Matches 157; Conservative 48; Mismatches 107; Indels 0; Gaps 0;
```

Db 191 GPECEYVRECEGELPLPOHVLNMCNCHPLGNFSFNOCSEFHCIDGYVNGSPKLEELASGIN 250  
QY 248 SSPEPTCOVIOCEPLASPDGIMNCSHPLASFSTTSACTFTCSGTEBLICKKKTICSSG 307  
Db 251 TNKRPQCLAAOCPLKIPERGNMTCLHSAKAFQHOSSCSCEGEGFALVGPVVOCTASG 310  
QY 308 IWSNPSPICOKL 319  
Db 311 VMTAPADVCKAI 322

RESULT 6  
095508  
ID 095508 PRELIMINARY; PRT; 740 AA.  
AC 095508;  
DT 01-MAY-1999 (TREMblrel. 10, Created)  
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
DE D1780M13.1.2 (SELECTIN P (GRANULE MEMBRANE PROTEIN 140 KDA, ANTIGEN CD62, GMP140)) (ISOFORM 2) (FRAGMENT).  
GN SELP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Howden P.;  
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL022146; CAA18143.1; -.  
DR HSSP; P16109; IKID.  
DR INTERPRO; IPR000436; -.  
DR INTERPRO; IPR000561; -.  
DR INTERPRO; IPR001304; -.  
DR INTERPRO; IPR002396; -.  
DR PFAM; PF00008; EGF\_1.  
DR PFAM; PF00059; lectin.C. 1.  
DR PFAM; PF00084; sushi; 8.  
DR PRINTS; PR00343; SELECTIN.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS00615; C\_Type\_Lectin\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50041; C\_Type\_Lectin\_2; 1.  
FT NON\_TER 740  
FT SEQUENCE 740 AA; 81389 MM; 1D2E35ED93745CE CRC64;

Query Match 42.4%; Score 898; DB 4; Length 740;  
Best Local Similarity 50.6%; Pred. No. 1.4e-79;  
Matches 158; Conservative 45; Mismatches 109; Indels 0; Gaps 0;

QY 8 QSTQDLMNIFKMGWMLCCDFLAHHGYCWTYHSEKPMNQRARFCRDNYTDVAI 67  
Db 11 QRFQVVFGLISQALISLITNOKREVAAMTYHSTKAYSWNISRKYCQNYTDLVAI 70  
QY 68 ONKAIELEYLEKTLTFFSRSYWIGIRKIGTWTGKSLTEEAENMGDEPNKKNKED 127  
Db 71 ONKMEIDYLMKVLPEYSYTWIGIRKKNKKTWTWGTAKKALITAEWMADEPNKKNKED 130  
QY 128 CVELIYIRKNDAGKWDADACHKLKALCYTASQCPWSCSGHGECEVELINHTCNCGVYX 187  
Db 131 CVELIYIRKNDAGKWDADACHKLKALCYTASQCPWSCSGHGECEVELINHTCNCGVYX 190  
QY 188 GPQCOLVIOCEPLASPDGIMNCSHPLASFSTTSACTFTCSGTEBLICKKKTICSSG 247  
Db 191 GPCEYVRECEGELPLPOHVLNMCNCHPLGNFSFNOCSEFHCIDGYVNGSPKLEELASGIN 250  
QY 248 SSPEPTCOVIOCEPLASPDGIMNCSHPLASFSTTSACTFTCSGTEBLICKKKTICSSG 307  
Db 251 TNKRPQCLAAOCPLKIPERGNMTCLHSAKAFQHOSSCSCEGEGFALVGPVVOCTASG 310  
QY 308 IWSNPSPICOKL 319

Db 311 HWSAPLPTCEAI 322

RESULT 7  
028290  
ID 028290 PRELIMINARY; PRT; 754 AA.  
AC 028290;  
DT 01-NOV-1996 (TREMblrel. 01, Created)  
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
DE CELL ADHESION MOLECULE PRECURSOR (FRAGMENT).  
GN GMP140.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Manning A.M., Sanders W.E. Jr., Kukielka G.L., Dore M.,  
RA Rosendloom C.L., Hawkins H.L., Michael L.H., Entman M.L., Smith C.W.,  
RA Beaudet A.L., Anderson D.C.;  
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; M88170; AAA63789.1; -.  
DR HSSP; P16109; IFSB.  
DR INTERPRO; IPR000436; -.  
DR INTERPRO; IPR000561; -.  
DR INTERPRO; IPR001304; -.  
DR INTERPRO; IPR002396; -.  
DR PFAM; PF00059; lectin.C. 1.  
DR PFAM; PF00084; sushi; 8.  
DR PRINTS; PR00343; SELECTIN.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS00615; C\_Type\_Lectin\_1; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS50041; C\_Type\_Lectin\_2; 1.  
FT Signal; Cell adhesion; glycoprotein.  
FT NON\_TER 1  
FT SIGNAL 1  
FT CHAIN 14  
FT SEQUENCE 754 AA; 82303 MM; F0438BEAA521E773 CRC64;

Query Match 41.8%; Score 884; DB 6; Length 754;  
Best Local Similarity 50.5%; Pred. No. 3.3e-78;  
Matches 151; Conservative 46; Mismatches 102; Indels 0; Gaps 0;

QY 19 KLMGWMLCCDFLAHHGYCWTYHSEKPMNQRARFCRDNYTDVAIONKARIEYLEK 78  
Db 7 KLICEVLIFFELIKQKEVAGWYNTSTKAYSMNYSRIFCOKHYTDVAIONKKEIATLND 66  
QY 79 TLFPSSYTWIGIRKIGTWTGKSLTEEAENMGDEPNKKNKEDCVELIYIRKND 138  
Db 67 VLPYNSYTWIGIRKINDKRWGVTGKPLTEEAENMAENEPNKNKQDCEIYIKSLA 126  
QY 139 AGKWDADACHKLKALCYTASQCPWSCSGHGECEVELINHTCNCGVYXPCQOLVIOCE 198  
Db 127 PGKWNDEPCWKRKRALCYTASQCPWSCSGHGECEVELINHTCNCGVYXPCQOLVIOCE 186  
QY 199 PLEAELCTMDCTHFGNFSFSQCAFSCSEGTNLTGIEFTTGGPFGNMSPPPTCOVIO 258  
Db 187 DFELPLPOHVLNMCNCHPLGNFSFNOCSEFHCIDGYVNGSPKLEELASGINTPRCVATQ 246  
QY 259 CEPISAPDGLGIMNCSHPLASFSTTSACTFTCSGTEBLICKKKTICSSGIMNSPPIQ 317  
Db 247 CPPLKTEPGQSMNCHLSEVAFQYQSSCHFSCEGEGFALVGPVVOCTASGWTAAAVCE 305  
RESULT 8  
029097  
ID 029097 PRELIMINARY; PRT; 646 AA.  
AC 029097;

DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)  
DE P-SELECTIN PRECURSOR.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OC NCBI\_TaxID=9823;  
RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=AORTA.  
RA Rollins S.A., Johnson K.K., Birks C.W., Matis L.A., Rother R.P.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=AORTA.  
RX MEDLINE=20171534; PubMed=10706724;  
RA Stocker C.J., Sugars K.L., Harari O.A., Landis R.C., Morley B.J.,  
Haskard D.O.;  
RT "TNF-alpha, IL-4, and IFN-gamma regulate differential expression of P-  
RT and E-selectin expression by porcine aortic endothelial cells.";  
RL J. Immunol. 164:3309-3315(2000).  
DR EMBL: L39075; AAA79007.1; -.  
DR EMBL: AF163766; AAF43272.1; -.  
DR HSSP: P16109; IFSB.  
DR INTERPRO: IPR000436; -.  
DR INTERPRO: IPR000561; -.  
DR INTERPRO: IPR001304; -.  
DR INTERPRO: IPR002396; -.  
DR PFAM: PF00008; EGF\_1.  
DR PFAM: PF00059; lectin\_C\_1.  
DR PFAM: PF00084; sushi; 6.  
DR PRINTS: PR00343; SELECTIN.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS00615; C-TYPE\_LECTIN\_1; UNKNOWN\_1.  
DR PROSITE: PS00186; EGF\_2; 1.  
DR PROSITE: PS50041; C-TYPE\_LECTIN\_2; 1.  
KW Signal; Lectin; Glycoprotein; Selectin.  
FT SIGNAL 1 41 POTENTIAL.  
FT CHAIN 42 646 P-SELECTIN.  
SQ SEQUENCE 646 AA; 71127 MW; 3863f4afe09f0db6 CRC64;

Query Match 41.4%; Score 876.5; DB 6; Length 646;  
Best Local Similarity 46.3%; Pred. No. 1, 5e-77;  
Matches 158; Conservative 48; Mismatches 124; Indels 11; Gaps 2;

QY 11 ORDLMNIFKLMGWTMLCCDFLAHHGTYCWTYHSEKPMNQARARFCRDNYTDLVAIONK 70  
DB 14 ORVSFRVQLLEFVALISDLNOKGVAAWYNYSTSAVSWNTSHVFCORYPTDLVAIONK 73  
QY 71 AEIYLEKTLPEFSRSYWGIRKGTGWTWGTNKSILTEAEENMGDEPNKKKKKECYE 130  
DB 74 KEIYALNDVILPYSSYWGIRKTKNNKWTGKTKTLQENNAKNEPNNSNNQDCE 133  
QY 131 IYIKRNDAKMDNDACHIKLKAALCTYASCPMSGSGHGECEVEIINNHCTCDVGYGPO 190  
DB 134 MYIKSLAPKGMNDPEVCRRKRALCYTASCSSTCSKQGETETIGVTCYSGFICPR 193  
QY 191 QALVIGCEPLAPBLGMDCTHPGPNFSFSQCAFSCSEGTNLGTEITTCGPGNMS 250  
DB 194 CEYKCEGEEFLPQYVLVLTNCSHPGPNFSFSQCAFSCSEGTNLGTEITTCGPGN 253  
QY 251 EPTQGVIGCEPLASPDGIMNCSHPLASFSTSACTFTCSGTELLKKKIKSSSGIMS 310  
DB 254 PPOCVAAVOCPLKSPKGNNAKCLHSEKAFDYOSSCNFSCEGVALYGEVVOAGSGMT 313  
QY 311 NPSPICOKLKSFSMIKEGDYNPFLTPVAVVTAFA-SGLAF 350  
DB 314 APYVCKAI-----ICEPLESPYRGSMDCFPSSRAF 344

RESULT 9

Q28657  
ID Q28657 PRELIMINARY; PRT; 649 AA.  
AC Q28657;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)  
DE P-SELECTIN.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OC NCBI\_TaxID=9986;  
RN  
RP SEQUENCE FROM N.A.  
RA Vora D.K., Fang Z., Liva S.M., Parham F., Watson A.D., Drake T.A.,  
RA Territo M.C., Berliner J.A.;  
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Marden C.H.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U39446; AAA81385.1; -.  
DR HSSP: P16109; IFSB.  
DR INTERPRO: IPR000436; -.  
DR INTERPRO: IPR000561; -.  
DR INTERPRO: IPR001304; -.  
DR INTERPRO: IPR002396; -.  
DR PFAM: PF00008; EGF\_1.  
DR PFAM: PF00059; lectin\_C\_1.  
DR PFAM: PF00084; sushi; 6.  
DR PRINTS: PR00343; SELECTIN.  
DR PROSITE: PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE: PS00615; C-TYPE\_LECTIN\_1; 1.  
DR PROSITE: PS00186; EGF\_2; 1.  
DR PROSITE: PS50041; C-TYPE\_LECTIN\_2; 1.  
KW Lectin; Glycoprotein.  
SQ SEQUENCE 649 AA; 71755 MW; ECCD8C847B84BC31 CRC64;

Query Match 40.7%; Score 860.5; DB 6; Length 649;  
Best Local Similarity 48.3%; Pred. No. 5, 6e-76;  
Matches 153; Conservative 53; Mismatches 104; Indels 9; Gaps 4;

QY 2 IFPKCOSTORDLMNIFKLMGWTMLCCDFLAHHGTYCWTYHSEKPMNQARARFCRDNY 61  
DB 8 IWMNR---FGAVRFTVQLLEFVALISDLNOKGVAAWYNYSTSAVSWNTSHVFCORYPTDLVAIONK 64  
QY 62 TDLVAIONKAEIYEKTLPEFSRSYWGIRK---IGIWTWGTNKSILTEAEENMGDE 118  
DB 65 TDLVAIONKNEIDVLENTIPYNSYWGIRKDOING--TWVG-NKMLTEAEENMADNE 121  
QY 119 PNKKRNKDECEIYIKRKKAADGKNNDACHIKLKAALCTYASCPMSGSGHGECEVEIINNH 178  
DB 122 PNKKRNNDCEIYIKSLAPGKMDPEVCRRKRALCYTASCSSTCSKQGETETIGVTCYSGF 181  
QY 179 TCNCDVGYGPOCQALVIGCEPLAPBLGMDCTHPGPNFSFSQCAFSCSEGTNLGTEITTC 238  
DB 182 TCSCYPRGYGPECEVEYRMAISDLRQHNHNMCSHPGPNFSFSQCAFSCSEGTNLGTEITTC 241  
QY 239 TTCGPGNMSDEPTCOVIGCEPLASPDGIMNCSHPLASFSTSACTFTCSGTELLKKKIKSS 298  
DB 242 LECIASGIMTSPQCVAAVOCPLKSPKGNNAKCLHSEKAFDYOSSCNFSCEGVALYGEVVO 301  
QY 299 KTIICESGIMSNPSITOKL 319  
DB 302 EVVHCTALGVTAFTPVCKAL 322

RESULT 10  
Q28982  
ID Q28982 PRELIMINARY; PRT; 482 AA.  
AC Q28982;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

Query Match	38.5%;	Score 815.5;	DB 6;	Length 482;
Best Local Similarity	36.1%;	Pred. No. 1e-11;		
Matches 159;	Conservative 56;	Mismatches 109;	Indels 117;	Gaps 7;

RESULT	11		
Q9VYR4			
ID	Q9VYR4	PRELIMINARY;	PRT, 1124 AA
AC	Q9VYR4;		
DT	01-MAY-2000	(TEMBREL. 13, Created)	

RP SEQUENCE FROM N.A.

RC STRAIN=BECKELEY;  
RA MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer J.R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abil J.F., Agayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Betman B.P., Bhandari D., Bolintsov S.,  
RA Borkova D., Botchan M.R., Bouck B., Brokstein P., Brotler P.,  
RA Burdits K.C., Busam D.A., Butler H., Cadieu E., Cantor A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Laspo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Llu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclio J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenhach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195(2000).  
DR EMBL: AF003487; AAF48125.1; -.  
DR HSSP: P02749; 10UB.  
DR FLYBASE: FBgn0001083; fw.  
DR INTERPRO: IPR000436; -.  
DR INTERPRO: IPR001304; -.  
DR PFAM: PF00059; lectin\_c; 1.  
DR PFAM: PF00084; sushi; 11.  
DR PROSITE: PS00615; C\_TYPE\_LECTIN\_1; 1.  
DR PROSITE: PSS0041; C\_TYPE\_LECTIN\_1; 1.  
SEQUENCE 1124 AA; 123051 MW; C0E0528A415F34A CRC64;

QY 38 CWTYHSELPNMMQRRFFCCNDNTDVAIONKAEIYEKLPSPRS-----YYWGIR 92  
 Db 231 CYDEHIT-KGESEFDMAQAIICKOTGSDLVHDFRCATSSYLSELBERKSELKPQLWIGAQ 269  
 QY 93 KIGGI-----WTYVGTGKSLTFEAEANMDGSPNNKKKECVITYIKRKNDAK--WNDD 145

Db 290 KEPGTSFTKWKVNGD---VVQKPTWKGDPNNNGEONCVL-----DGGRNLMNDV 340  
QY 146 ACHKLKALCYTASQPMSCSGH-----GECVEIT-----NNHTC 180  
Db 341 GCN--LDVLFHTICQHSPLSCSPDAQONTYWGKKFTLGEKIQTICPFGHSLGTEREC 398  
QY 181 NCDVGYVG--PQCOLVIOCEPLEAELGTMDCTHPFGNF-----SFSOCAFSCSEGT 231  
Db 399 RLDGTWSSSPTCKYV--DCGSL--PEL-----KFGSIHSEKTSFGVATYSCHENY 448  
QY 232 NLTGIEFTTCGPFQWSSPEPTCOYIQC--EPLSAPLGLIMNCHPLASFSFT-----S 283  
Db 449 TLIGENNTKCAMDG--WSGKQPECLVDMCPDPPPIAGDV-----RFNDKRAGS 495  
QY 284 ACTFICSEGTGICGKKTKICSSGIMSNPSPICOKLD 320  
Db 496 TATVCEPGYVLVGEALITSCGIGEMSSKTPSCRRVD 532

## RESULT 12

P91658 PRELIMINARY; PRT; 974 AA.

AC P91658.  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE FURROEMD.  
CN FW.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_Taxid=7227;  
RN RN  
RP SEQUENCE FROM N.A.  
RA Leshko-Lindsay E., Corces V.G.;  
RL Development 0:0-0(0).  
DR EMBL: U70770; AAB36703.1; -.  
DR HSSP: P02749; 10UB.  
DR FLYBASE; FBgn0001083; fw.  
DR INTERPRO; IPR000436; -.  
DR INTERPRO; IPR001304; -.  
DR PFAM; PF00059; lectin\_c.1.  
DR PFAM; PF00084; sushl; 10.  
DR PROSITE; PS00615; C-type\_lectin\_1; UNKNOWN\_1.  
DR PROSITE; PS50041; C-type\_lectin\_2; 1.  
SQ SEQUENCE 974 AA; 107557 MW; A406335FB6726757 CRC64;

Query Match 11.2%; Score 237.5; DB 5; Length 974;

Best Local Similarity 25.2%; Pred. No. 1.2e-14;

Matches 85; Conservative 39; Mismatches 124; Indels 89; Gaps 18;

QY 38 CWTYHYSEKPMNWDARFRCDNTDLVAIONKAEIYELEKTLPEFSRS---YWGIR 92  
Db 49 CYDFHIT-KGSFKAQIKQKOTGHLVDFRGATSSYILSELEKRSKELKPOLWIAQ 107  
QY 93 KIGGI-----WTVGINKSLTEAENMGDEPERNNKKNKEDCEIYIKRKKDAGK---WMD 145  
Db 108 KEPGTSFTKWKVNGD---VVQKPTWKGDPNNNGEONCVL-----DGGRNLMNDV 158  
QY 146 ACHKLKALCYTASQPMSCSGH-----GECVEIT-----NNHTC 180  
Db 159 GCN--LDVLFHTICQHSPLSCSPDAQONTYWGKKFTLGEKIQTICPFGHSLGTEREC 216  
QY 181 NCDVGYVG--PQCOLVIOCEPLEAELGTMDCTHPFGNF-----SFSOCAFSCSEGT 231  
Db 217 RLDGTWSSSPTCKYV--DCGSL--PEL-----KFGSIHSEKTSFGVATYSCHENY 266  
QY 232 NLTGIEFTTCGPFQWSSPEPTCOYIQC--EPLSAPLGLIMNCHPLASFSFT-----S 283  
Db 267 TLIGENNTKCAMDG--WSGKQPECLVDMCPDPPPIAGDV-----RFNDKRAGS 313

QY 284 ACTFICSEGTGICGKKTKICSSGIMSNPSPICOKLD 320  
Db 314 TATVCEPGYVLVGEALITSCGIGEMSSKTPSCRRVD 350

## RESULT 13

ID18849 PRELIMINARY; PRT; 868 AA.

AC Q18849.  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE C54G4.4 PROTEIN.  
GN C54G4.4.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_Taxid=6239;  
RN RN  
RP SEQUENCE FROM N.A.  
RA Wilkinson J.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Cosey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Lalster N., Latellie P.,  
RA Lightling J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,  
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Sprat J., Woldman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
DR EMBL: Z75533; CA99822.1; -.  
DR INTERPRO; IPR000436; -.  
DR INTERPRO; IPR001304; -.  
DR PFAM; PF00084; sushl; 4.  
DR PROSITE; PS50041; C-type\_lectin\_2; 1.  
SQ SEQUENCE 868 AA; 95322 MW; 5D57C32C70405CD CRC64;

Query Match 11.2%; Score 236; DB 5; Length 868;

Best Local Similarity 22.3%; Pred. No. 1.4e-14;

Matches 84; Conservative 48; Mismatches 128; Indels 116; Gaps 18;

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Db 339 VSPWQCAOSQMEVGVF-----GGMCTAASRDQ-TDWLQAQRKCLDRG 381  
QY 62 TDLVAIONKAEIYELEKTLPEFS---RSYWGIRKIGIKWTVGNTKSLTEAENMGD-- 116  
Db 382 STLPLRIDDSRRGIRLSALSSASSAKAFYWGICASSMTEMWV-----DGEVYGSA 433  
QY 117 ---GEPNNKKNKEDCEI-----YIKRKNKADKWDACHKILKALCYTASQPMSCS 166  
Db 434 DMPGQSPSPASAEVLLARPLEWKPVASQTA--WNSFLQS-KPKRC-----TSP 482  
QY 167 GHGCEVEL-TNNHT-----C--NCDVY-----YGHOCV 194  
Db 483 GVGATKYVTFSSHSAIGITLCFYSDSGYDLHGIRQRCANGHWGTSIPNCRKSCAV 542  
QY 195 IQCELEAELGTMDCTHPFGNFS-----SFSOCAFSCSEGTNLGIEFTT----- 240  
Db 543 RQWK-----FGRIKLNTTLFESVEYETGSGNHLNANSPSTYRSLRV 587  
QY 241 CGPFGNWSPEPTCOYIQCPEPLSAPLGLIMNCHPLASFSFTACTFICSEGTGICKK 300  
Db 588 COSDGIWGSSEPTCELVDG---GRPPL-IANGRVDESSSTESANANYCHQGFRIGES 643

QY 301 TICSSSGTWSNPIC 316  
 Db 644 LMGDRGEMOPATPFC 659

RESULT 14  
 QYVXX7  
 ID QYVXX7 PRELIMINARY; PRT; 1061 AA.  
 AC QYVXX7;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
 DE CG9095 PROTEIN.  
 GN CG9095.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Phylodoidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxId=7227;  
 RN [1]  
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 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iibegwan C.,  
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Meltel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spter E., Spreading A.C., Stapleton M., Strong R., Sun E.,  
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003498; AAF48429.1; -;  
 DR FLYBASE: FBgn0030617; CG9095.  
 DR INTERPRO: IPR000436; -;  
 DR INTERPRO: IPR001304; -;  
 DR INTERPRO: IPR003006; -;  
 DR PFAM: PF00084; lectin\_3; 1.  
 DR PFAM: PF00084; sushi\_3;  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN.1.  
 DR PROSITE: PS00615; C\_TYPE\_LECTIN.1; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LECTIN.2; 1.  
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 Best Local Similarity 24.2%; Pred. No. 1.6e-12;  
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 QY 85 SYTWGIGRIG---GIMTWV-GTKNSLLEAEENNGDGEPPNKKKEDCVETLYIKRNKDG 140  
 Db 232 SQYMWGAVRQSDSSSMKWVNGDELIVSFWSHPGSD-----EDCARF-----DCS 276  
 QY 141 K---WNDACRKLKALCYTASCQWSCSGHGE-----CVEIIN-----NH 178  
 Db 277 KGLWSDTNCNTLNFIC---QHQPKC-GRPEDGPSTWALNGEYVGAQIYSCDANH 332  
 QY 179 -----TNCQDVGYG---PQCQLYIQCPLEAPELGTMDCRHP---FGNFS-----218  
 Db 333 LLVGPATRTC-LETGFYNEPPVCKYI-----ECGLPASIAHGSYALNNNT 377  
 QY 219 --FSSQAFSCSEGTNLTGLEETCGFGNWSPEPTCOVIOCEPLSAPDLG-IMNCSPH 275  
 Db 378 VGYLSLVKYSCEBGEYEMIGRALLTCDDERWNGPPRCCEIVEDDTLPNGVYTTINA--P 435  
 QY 276 LASSFSFACFTFSEGTETLIGKKTTICSSGIMSNPSPICOKLIDKS 322  
 Db 436 NGTY-YGSKAEIISCPGYPGRMEGRVYLICLASGWSALPRCITLERS 481

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 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)  
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 GN HF OR CFH.  
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 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86134059; PubMed=2963625;  
 RA Ripoché J., Day A.J., Harris T.J.R., Sim R.B.;  
 RL "The complete amino acid sequence of human complement factor H.";  
 RL Biochem. J. 249:593-602(1988).  
 RN [2]  
 RP SEQUENCE OF 226-449 FROM N.A.  
 RX MEDLINE=86169701; PubMed=2937845;  
 RA Kristensen T., Wetzel R.A., Jack B.F.;  
 RT "Structural analysis of human complement protein H: homology with C4b  
 RT binding protein, beta 2-glycoprotein I, and the Ba fragment of B2.";  
 RL J. Immunol. 136:3407-3411(1986).  
 RN [3]  
 RP SEQUENCE OF 1-19 FROM N.A.  
 RA Vik D.P., Williams S.A.;  
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-9 FROM N.A.  
 RA Dominguez O.;  
 RL Thesis (1993); Immunologia, Hospital Trias I Pujol, Spain.  
 DR EMBL: X07523; CA030403.1; -;  
 DR EMBL: M12383; AAA52013.1; -;  
 DR EMBL: U56979; AAB01987.1; -;  
 DR EMBL: Z29665; CAA82763.1; -;  
 DR HSSP: P10988; IYVD.  
 DR INTERPRO: IPR000436; -;  
 DR PFAM: PF00084; sushi\_7.  
 KW Signal.

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Best Local Similarity	25.88;	Pred. No. 2.4e-11;		
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QY      189  --PCQOLVIOCEPLAEPLIGM--DCHHPGNSFSSQCAFSCSEGNLTGIEETTCGP 244
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QY      245  GNMWSPPEPCVIOICEPLSLAPDLGIMNCSHPLAS--FSETSACTFICSEGTLEIKKKT 301
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QY      302  ICSSSGIMSNPSPTCKQLUDLSFSMIKRGCVINPLFI 336
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/lab_host="DH10B"
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T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and Eco RI
the Not I and Eco RI sites of the modified p773 vector.
Library is normalized, and was constructed by Bento
Soares and M.Felina Bonaldo."
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Baylor-HMSC project=TCBA Homo sapiens cDNA clone TCBAPEI1956, mRNA
sequence.
BE245855
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KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 416)
Mel.Y., Tsang.Y.T.M., Mei.G., Ku.J.M., Ali-Osman Jr., F.R., Muzny,D.,
Bonick,J.F., Gibbs,R.A. and Margolin,J.F.
Pediatric leukemia cDNA sequencing Project

```

JOURNAL Unpublished (2000)  
 COMMENT Contact: Dr. Judith F. Margolin  
 Human Genome Sequencing Center at Baylor College of Medicine and  
 Texas Children's Cancer Center  
 One Baylor Plaza, Houston, TX 77030, USA  
 Tel: 713 770 4536  
 Fax: 713 770 4038  
 Email: jmargin@tccc.org  
 Seq primer: M13 primer.

FEATURES  
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 3'; V-A,C,G; N-A,C,G,T] and then dg tailed. Second  
 strand was primed with a BamHI-dc primer  
 [5'AGAGCTCGATCGCGGCCGCAATATATAT(C) 3'].  
 Double-stranded cDNA was then digested with BamHI and  
 XhoI and directionally cloned into the BamHI and SalI  
 sites of lambda PSB vector. Library went through one  
 round of normalization. Library was constructed by Wei  
 Yu"

BASE COUNT 123 a 87 c 110 g 95 t 1 others

ORIGIN

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Align seg 1/1 to: BE245855 from: 1 to: 416

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101 Val 101
|||
413 GTG 415
```

seq\_name: gb\_est68:BE246681

seq\_documentation\_block:  
 LOCUS BE246681 421 bp mRNA EST 13-JUL-2000  
 DEFINITION TCBAP1E5091 pediatric pre-B cell acute lymphoblastic leukemia  
 Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP5091, mRNA  
 sequence.

ACCESSION BE246681  
 VERSION BE246681.1 GI:9098430  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 AUTHORS Wei,Y., Tsang,Y.T.M., Mel,G., Xu,J.M., Ali-Osman Jr.,F.R., Muzny,D.,  
 Bouck,J., Gibbs,R.A. and Margolin,J.F.  
 TITLE Pediatric leukemia cDNA Sequencing Project  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Dr. Judith F. Margolin  
 Human Genome Sequencing Center at Baylor College of Medicine and  
 Texas Children's Cancer Center  
 One Baylor Plaza, Houston, TX 77030, USA  
 Tel: 713 770 4536  
 Fax: 713 770 4038  
 Email: jmargin@tccc.org  
 Seq primer: M13 primer.

FEATURES  
 source Location/Qualifiers  
 1. 421  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_id="TCBAP5091"  
 /clone\_lib="Pediatric pre-B cell acute lymphoblastic  
 leukemia Baylor-HGSC project-TCBA"  
 /sex="male"  
 /tissue\_type="leukopheresis"  
 /cell\_type="pre-B cell"  
 /dev\_stage="pediatric 2 years"  
 /lab\_host="DH10B"  
 /note="Vector: lambda PSB. Site\_1: BamHI; Site\_2: EcoRI;  
 First strand cDNA was primed with an anchored  
 XhoI-oligo(dT) primer [5'GAGAGCTCGACGCCGCCGAGAGAG(T)VN  
 3'; V-A,C,G; N-A,C,G,T] and then dg tailed. Second  
 strand was primed with a BamHI-dc primer  
 [5'AGAGCTCGATCGCGGCCGCAATATATAT(C) 3'].  
 Double-stranded cDNA was then digested with BamHI and  
 XhoI and directionally cloned into the BamHI and SalI  
 sites of lambda PSB vector. Library went through one  
 round of normalization. Library was constructed by Wei  
 Yu"

BASE COUNT 118 a 99 c 108 g 95 t 1 others

ORIGIN

alignment\_scores:  
 Quality: 554.00 Length: 97  
 Ratio: 5.771 Gaps: 0  
 Percent Similarity: 98.969 Percent Identity: 96.907

alignment\_block:  
 US-09-119-209-2 x BE246681 ..

Align seg 1/1 to: BE246681 from: 1 to: 421

```

1 MetlllePhePrrPlyScysGlnSerThrGlnArGAsPleUTrPAsn11 17
|||||
114 ATGATATTTCATGCAATGTCAGAGCACCCAGAGGACATTATGGAACAT 163
17 ePhelysLeuTrpGlyTrpThrMetLeuCysAspPheLeuAlaIsh 34
|||||
164 CTTCAGTTGGGGGTGGACAATGCTGTGTGATTTCTGGGACATC 213
```

```

34  ISGlyThrTyrCysThrTyrHisTyrSerGluYsPrometAsnTrp 50
|||||
214 ATGGAACCGACTGCTGACTTACCATTTCTGAAAAACCATGAACCTGG 263
51  GlnArgAlaArgArgPheCysArgAspAsnTyrThrAspLeuValAlaI 67
|||||
264 CAAGGGGCTAGAGATCTTCCGAGACAAATTACACAGATTAGTGCAT 313
67  eGlnAsnLysAlaGluIleGluTyrLeuGluYsThrLeuProPheSer 84
|||||
314 ACAAAACAGAGCGGAATGTGATATCTGAGAGAAAGACTGCTTCATGCT 363
84  rGSerTyrTyrPheIleGlyIleArgLysIleGlyIle 97
|||||
364 GTTCTTACTACTGATAGATCCGCGCATAGAGAGACTA 404
seq_name: gb_est28:AL047443

```

```

seq_documentation_block:
LOCUS      AL047443      599 bp      mRNA      EST      29-FEB-2000
DEFINITION DKFZP586J1120_r1 586 (synonym: hute1) Homo sapiens cDNA clone
ACCESSION  AL047443
VERSION    AL047443.1 GI:4727358
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 599)
AUTHORS   Wambuit,R., Heubner,D., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE      EST (Wambuit, et al.)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Wambuit R
            MIPS
            Am Klopferplatz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert
            clone from S. Wiemann, Molecular Analysis, German Cancer
            Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
            consortium of the German Genome Project.
            No s1 sequence available.
            This clone (DKFZP586J1120) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
Source     1..599
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="DKFZP586J1120"
            /clone_lib="586 (synonym: hute1)"
            /tissue_type="uterus"
            /dev_stage="adult"
            /lab_host="DH10B"
            /note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"
BASE COUNT 162 a 138 c 159 g 139 t 139 others
ORIGIN

```

```

alignment_scores:
Quality: 553.00      Length: 189
Ratio: 3.814         Gaps: 0
Percent Similarity: 76.720 Percent Identity: 49.206

```

```

alignment_block:
US-09-119-209-2 x AL047443 ..

```

```

Align seg 1/1 to: AL047443 from: 1 to: 599

```

```

129 ValGluIleTyrIleLysArgAsnLysAspAlaGlyLysTyrAsnAspAs 145
|||||
1 GTGAGATCTTACTCAAGAGAAAAAGATGTGGCATGTGGAAATGATGA 50

```

```

145 pAlaCysHisLysLeuLysAlaAlaLeuCysTyrThrAlaSerCysGln 162
|||||
51 GAGGTGCAGCAAGAAAGACCTTGCCCTATGCTACACAGACTGCTGTACCA 100
162 rOTrPserCysSerGlyHisGlyGluCysValGluIleIleAsnAsnHis 178
|||||
101 ATATACATCCGCGAGTGGCCAGGTGATGTGTAGAGACCATTAAATTAATTC 150
179 ThrCysAsnCysAspValGlyTyrTyrGlyProGlnCysGlnLeuValI 195
|||||
151 ACTTGCAAGTGTGACCCCTGCTGAGTCAAGTCAAGTGTGACAAATTTGT 200
195 eGlnCysGluProLeuGluAlaProGlnLeuGlyThrMetLaspCysThr 212
|||||
201 GAACGTGTACAGCCCTGGAATCCCTGAGACATGAGAACGCTGTGTGCATC 250
212 isProPheGlyAsnPheSerPheSerSerGlnCysAlaPheSerCysSer 228
|||||
251 ACCCACTGGAAACTTCAGTCACAAATTTCTGCTATACAGCTGTGAT 300
229 GluGlyThrAsnLeuThrGlyIleGluGluThrThrCysGlyProPheG 245
|||||
301 AGGGGTACCTGCGCAAGCATGAGACCATGCATGCATGTCCTCTCTGCG 350
245 YAsnTrpSerSerProGluProThrCysGlnValIleGlnCysGluProL 262
|||||
351 AGAATGAGAGTCTCTTATTCAGCTGCAATGTGTGAGTGTGATGCTGCG 400
262 euSerAlaProAspLeuGlyIleMetAsnCysSerHisProLeuAlaSer 278
|||||
401 TGACAAATCCAGCAATGGGTGTGTGGAATGTTCCAAAAACCTGGAAAC 450
279 PheSerPheThrSerAlaCysThrPheIleCysSerGluGlyThrGlu 295
|||||
451 TTCACATGAGAACACAACTGTGATTTGACTGTGAAGAAGATTTGAACT 500
295 uIleGlyLysLysLysThrIleCysGluSerSerGlyIleTrpSerAsn 312
|||||
501 AATGGGAGCCCAAGCCCTTACGTGTACCTCATCTGTGGAAATTGGGACAC 550
312 roSerProIleCysGln 317
|||||
551 AGAAGCCAAACGCTGTAA 567
seq_name: gb_est6:AA355761

```

```

seq_documentation_block:
LOCUS      AA355761      293 bp      mRNA      EST      21-APR-1997
DEFINITION EST64209 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
selectin L, mRNA sequence.
ACCESSION  AA355761
VERSION    AA355761.1 GI:2008079
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 293)
AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fullmer,R.A., Bult
            ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
            ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Well,C., Clayton,R.A.,
            Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,
            ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodek,A.,
            Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
            Kelley,J.C., Liu,L.-I., Marnaros,S.M., Merrick,J.M.,
            Moreno-Palagunes,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,
            Smill,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrite,A., Fischer,C., Hastings,G.A., He,W.W.,
            Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
            Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
            Wei,T.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon

```

TITLE  
JOURNAL  
MEDLINE  
COMMENT

,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and  
Venter,J.C.  
Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cDNA sequence  
Nature 377 (6547 Suppl), 3-174 (1995)  
96026280  
Other-ESTs: YHC172390  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlavage@igf.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.

FEATURES  
source  
1. .293  
/organism="Homo sapiens"  
/db\_xref="ATCC (inhost):157887"  
/db\_xref="taxon:9606"  
/clone\_lib="Jurkat T-cells VI"  
/cell\_type="T-lymphocyte"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
XhoI"

BASE COUNT  
ORIGIN  
70 a 71 c 75 g 74 t 3 others

alignment\_scores:  
Quality: 547.00 Length: 97  
Ratio: 5.758 Gaps: 0  
Percent Similarity: 97.938 Percent Identity: 94.845

alignment\_block:  
US-09-119-209-2 x AA355761 ..

Align seg 1/1 to: AA355761 from: 1 to: 293

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160 CysGlnProTTPSerCysSerGlyHisGlyGlyCysValGluIleIleAs 176
|||||
3 TGCCAGCCCTGGTCAATGCAGTGGCCATGCGAATGTGTAGANNATCAATCAA 52
176 nasnhisthrcysasnrcysaspvalgltgtytrtyrclgtyproglncysglnl 193
|||||
53 TAAATACACCTGCACATGTGATGTGGGTACTATGCGCCACAGTGTCACT 102
193 euvalilcglncysgluproleugluAlaProgluLeuGlyThrmMetasp 209
|||||
103 TTGTGATTCAGGTGAGCGCTTTGGAGGCCCCAGAGCTGGGTTCCTGAGNC 152
210 CysThrHisProPheGlyAsnPheserPheserSerGlnCysAlaPhase 226
|||||
153 TGTACTACACCCCTTTGGAAACTTTCAGCTTCACAGTGCAGTGTGCTTCAG 202
226 rcyssercluglythrpsanleuthrglytlegluGluThrTrpCysGly 243
|||||
203 CTGCTCTAGACGAACAACCTTAACCTGGGATTGAGAAACACACCTCTGGAC 252
243 rophegLYAsnTrpSerSerProgluProThrCysGlnVal 256
|||||
253 CATTTGGAAACTGCTCATCTCCAGAACCAACACCTGTCAAGTG 293

```

seq\_name: gb\_est43:AW314314

seq\_documentation\_block:  
LOCUS AW314314 382 bp mRNA EST 09-JUL-2000  
DEFINITION 10316 MARC 2Pig Sus scrofa cDNA 5', mRNA sequence.  
ACCESSION AW314314  
VERSION AW314314.1 GI:6743570  
KEYWORDS EST.

SOURCE  
ORGANISM

pig.  
Sus scrofa

REFERENCE  
AUTHORS

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
1 (bases 1 to 382)  
Fahrenkrug,S.C., Fekling,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,  
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.  
and Keeler,J.W.

TITLE  
JOURNAL  
COMMENT

Design and use of two pooled tissue normalized cDNA libraries for  
EST discovery in swine  
Unpublished (2000)  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390

Email: [smith@email.marc.usda.gov](mailto:smith@email.marc.usda.gov)  
Single pass sequencing. Bases called and trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -mnscore 20  
and -mismatch 12 options.

PCR primers:  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCAGTCACGACG  
Plate: 7 row: P column: 14  
Seq primer: ATTTCAGTGCACACTATAC.  
Location/Qualifiers  
1. .382  
/organism="Sus scrofa"  
/db\_xref="taxon:9823"  
/clone\_lib="MARC 2Pig"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from testis, ovary,  
endometrium, hypothalamus, pituitary, and placenta."

BASE COUNT  
ORIGIN  
105 a 68 c 111 g 98 t

alignment\_scores:  
Quality: 509.00 Length: 102  
Ratio: 5.247 Gaps: 0  
Percent Similarity: 95.098 Percent Identity: 81.373

alignment\_block:  
US-09-119-209-2 x AW314314 ..

Align seg 1/1 to: AW314314 from: 1 to: 382

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1 MetIlePheProTTPTrpCysGlnSerThrglnATGAspLeuTrpAsn11 17
|||||
77 ATGATATTTCCATGAGAAATGTGCACAGTGTCTCAGAGGGCTTATGGAAATGT 126
17 ePheLysLeuTrpGlyTrpThrmLeuCysCysAspPheLeuAlaIle18 34
|||||
127 CTTCAGAGTTGTGGTGGTCCGACATATGCTTTGTGTGATTTTGTTCATATTC 176
34 lsgLYThrTyrCysTrpThrTrpThrHisTyrSerGlnLysProMetAsnTrp 50
|||||
177 ATGCAACGTGATTCGTGACATTCACACTATTCGAAAAACCCATGAACTCG 226
51 GlnATGAlaATGATGPhcCysATGAspAsnTyrTrpAspLeuValAla11 67
|||||
227 ATGAGAGCTAGGAAGTTCTGTGCAGAAATTTACACAGATTTGGTGGCATT 276
67 eGlnAsnLysAlaGluIleGluTyrLeuGluLysThrLeuProPheSerA 84
|||||
277 ACAAAACAAGGGGAGATTTGAATACCTGAATTAAGACGCTTCCCTTCACAGC 326
84 rGSerTyrTyrTrpIleGlyIleATGlysIleGlyGlyIleTrpThrTrp 100
|||||
327 GTAGTTACTACTGATAGGAATCCGGAAGTGTGAGAGGGGTATGACATTGG 376

```



```
source
1. .282
/organism="Homo sapiens"
/db_xref="ATCC (inhost):165681"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; site_1: EcoRI; site_2: XhoI"

BASE COUNT      71 a      73 c      64 g      73 t      1 others
ORIGIN

alignment_scores:
Quality: 501.00      Length: 92
Ratio: 5.505      Gaps: 0
Percent Similarity: 98.913      Percent Identity: 96.739

alignment_block:
US-09-119-209-2 x AA361531 ..

Align seg 1/1 to: AA361531 from: 1 to: 282

204 GUGUGUgUThrMetAspCysThrHisProPheGlyAsnPheSerPhe 220
|||||
1 GAGCTGGGgTACCATGACTGACTGACCTTGGGAACTTCACTGAGCTTCA 50
220 rSerGlnCysAlaPheSerCysSerGlnGlyThrAsnLeuThrGlyIle 237
|||||
51 CTCACAGTGTGCTTCAGCTGCTCTGAGAGAACAACTTAACCTGGGATTG 100
237 luGluThrThrCysGlyProPheGlyAsnTrpSerSerProGluProThr 253
|||||
101 AAGAAGCCACCTGTGACCATTTGGAACTGTCATCTCCAGAACCAACC 150
254 CysGlnValIleGlnCysGluProLeuSerAlaProAspLeuGlyIle 270
|||||
151 TGTCAGGATTCATCANTGTGAGCCTCTATCCAGCACAGATTGGGATCAT 200
270 vaNcysSerHisProLeuAlaSerPheSerPheThrSerAlaCysThrP 287
|||||
201 GAACGTGTACCCATCCCTGCGCCAGCTTTCAGCTTTCCTGCACTGACT 250
287 heileCysSerGlnGlyThrGluLeu 295
|||||
251 TCATCTGCTCAGACAGAACTGAGGTT 276

seq_name: gb_est44:AM408490

seq_documentation_block:
LOCUS      AM408490      551 bp      mRNA      EST      16-FEB-2000
DEFINITION UT-HF-BKO-abm-g-01-0-UT.r1 NIH_MGC_36 Homo sapiens cDNA clone
IMAGE:3056832 5', mRNA sequence.
ACCESSION  AM408490
VERSION    AM408490.1 GI:6927547
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     unpublished (1999)
JOURNAL   Contact: Robert Strausberg, Ph.D.
COMMENT   Tel: (301) 496-1550
          Email: Robert.Strausberg@nih.gov
          Eco RI site shown at the beginning of the sequence.
          Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
          cDNA Library Preparation: M.B. Soares Lab
          cDNA Library Arrayed by: M.B. Soares Lab
          DNA Sequencing by: M.B. Soares Lab
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
```

```
www.bio.llnl.gov/bdrrp/image/image.html
Seq primer: M13 Forward.
FEATURES
source
1. .551
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:3056832"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pTT3-Pac; site_1: NotI; site_2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D., and M. Bento Soares, Ph.D."

BASE COUNT      162 a      124 c      106 g      159 t
ORIGIN

alignment_scores:
Quality: 496.00      Length: 94
Ratio: 5.277      Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-119-209-2 x AM408490 ..

Align seg 1/1 to: AM408490 from: 1 to: 551

279 PheSerPheThrSerAlaCysThrPheIleCysSerGlnGlyThrGlu 295
|||||
9 TTCAGCTTTTACCTCTGATGATGACTTTCATCTGCTCGAAGAGAACTGAC 58
295 uIleGlyLysLysLysThrIleCysGlnSerSerGlyIleTrpSerAsn 312
|||||
59 AATTGGAGAGAGAAAGAAACCATTTGTGATCATCTGATCTGGTCAATTC 108
312 roSerProIleCysGlnLysLeuAspLysSerPheSerMetIleLysGlu 328
|||||
109 CTAGTCCAAATATGTCAAAATTTGGACAAAGTTTCCATGATTAAGAG 158
329 GlyAspTrpAsnProLeuPheIleProValAlaValMetValThrAla 345
|||||
159 GGTGATTATTAACCCCTCTTTCATTCAGTGGCAGTCATGCTACTGCATT 208
345 eSerGlyLeuAlaPheIleIleTrpLeuAlaArgLeuLysGlyL 362
|||||
209 CTCTGGGTGGCATTTATCATTTGGCTGGCAGAGATTAAGGCA 258
362 yAlaSerLysArgSerMetAsnAspProTyr 372
|||||
259 AGAAATCCCAAGAGAGATGATGATGATGATGATGATGATGATGATGAT 290

seq_name: gb_est39:AM075834

seq_documentation_block:
LOCUS      AM075834      632 bp      mRNA      EST      13-OCT-1999
DEFINITION xa80C03.x1 NCI-CGAP_CM11 Homo sapiens cDNA clone IMAGE:2573092 3'
similar to gb:U16150_cds1 L-SELECTIN PRECURSOR (HUMAN); mRNA
sequence.
ACCESSION  AM075834
VERSION    AM075834.1 GI:6030832
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE     Tumor Gene Index
```

JOURNAL  
COMMENT

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Tel: (301) 496-1550  
Email: Robert.Strausberg@nih.gov  
Tissue Procurement: Elisabeth Paletta, Jonathan D. Licht, M.D.,  
Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life  
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The  
I.M.A.G.E. Consortium DNA Sequencing by: Washington University  
Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMW at:  
www.bio.lnlnl.gov/bdnp/image/image.html  
Seq primer: -400P from Glibco  
High quality sequence stop: 147.

## FEATURES

source

1..632  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2573092"  
/clone\_lib="NCI-CCAP CML1"  
/tissue\_type="myeloid cells, 18 pooled CML cases, BCR/ABL  
rearrangement positive, includes both chronic phase and  
myeloid blast crisis"  
/lab\_host="DH10B"  
/note="Organ: whole blood; Vector: pCMV-SPORT6; Site\_1:  
Salt: Site\_2: NotI; Cloned unidirectionally. Primer:  
Oligo dT. Library constructed by Life Technologies."  
BASE COUNT 175 a 126 c 130 g 201 t  
ORIGIN

alignment\_scores:  
Quality: 452.00 Length: 99  
Ratio: 4.809 Gaps: 0  
Percent Similarity: 94.949 Percent Identity: 91.919

## alignment block:

US-09-119-209-2 x AM075834/rev ..

Align seg 1/1 to reverse of: AM075834 from: 1 to: 632

```

271 AsncysSerHisProLeuAlaSerPheSerPheThrSerAlaCysThrPh 287
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
616 GACGTACACCATCCTTGCCAGCTCAAGCTTACCTCGAATGACCTC 568
287 eLecysSerGluGlyThrGluLeuIleGlyLysLysLysThrIleCysG 304
567 .ATCGCTCAGAGAACTGAGTTAATGGAGAGAAACCATTTGTG 518
304 LuserSerGlyIleTrpSerAsnProSerProIleCysGlnLysLeuAsp 320
517 AATCATCTGGAATCTGCTCAATCTTACCTCAATATGCAAAATTTGGAC 468
321 LysSerPheSerMetIleLysGluGlyAspTyrAsnProLeuPheIlePr 337
467 AAAAGTTTCTCAATGATTAAAGAGGGGATATATACCCCTTCATTCC 418
337 oValAlaValMetValThrAlaPheSerGlyLeuAlaPheIleIleTrpL 354
417 AGTGGCAGTCAATGTTACTGATCTCTGGGTTGCAATTTATCATTTGGC 368
354 euAlaArgArgLeuLysGlyLysLysSerLysArgSerMetAsn 369
367 TGGCAAGGAGATTAAAAAGGCAAGAAATCCAGAGAGAGATTGAT 321
seq_name: gb_est6:AA355788

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seq\_documentation\_block: 346 bp mRNA EST 21-APR-1997  
LOCUS AA355788  
DEFINITION EST64242 Jurkat T-cells VI Homo sapiens CDNA 5' end similar to  
selectin L, mRNA sequence.  
ACCESSION AA355788  
VERSION AA355788.1 GI:2008107

## KEYWORDS

ESF  
SOURCE

## ORGANISM

human.

## REFERENCE

## AUTHORS

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulton, R.A., Bult  
, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White  
, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, M., Clayton, R.A.,  
Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fink, L.D., Fitzgerald  
, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodek, A.,  
Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M.,  
Kelley, J.C., Liu, L.-I., Marmaro, S.M., Merrick, J.M.,  
Moreno-Palmer, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,  
Phillips, C.A., Ryder, S.E., Scott, D.L., Sauder, D.M., Shirley, R.,  
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,  
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,  
Dimke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A., He, W.W.,  
Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,  
Kunsch, C., Hung, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L.,  
Wei, T.F., Ming, J., Xu, C., Yu, G., L., Ruben, S.M., Dillion, P.J., Fannon  
, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and  
Venter, J.C.  
TITLE Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of CDNA sequence  
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
MEDLINE 96026280  
COMMENT Other-ESTs: TNC172390  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tldb/hgi/hgi.html>)  
Seq primer: M13 Reverse

## FEATURES

source

1..346  
Location/Qualifiers

/organism="Homo sapiens"  
/db\_xref="ATCC (Inhost):157916"  
/db\_xref="taxon:9606"  
/clone\_lib="Junkat T-cells VI"  
/clone\_type="T-lymphocyte"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
XhoI"  
BASE COUNT 102 a 75 c 86 g 80 t 3 others  
ORIGIN

alignment\_scores:  
Quality: 437.00 Length: 83  
Ratio: 5.675 Gaps: 1  
Percent Similarity: 92.771 Percent Identity: 92.771

## alignment block:

US-09-119-209-2 x AA355788 ..

Align seg 1/1 to: AA355788 from: 1 to: 346

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1 MetIlePheProTrpLysCysGlnSerThrGlnArgAspLeuTrpAsnL 17
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96 ATGATATTTCCATGGAATGTCAGAGACCCAGAGGAGACTTATGGAACAT 145
17 ePheLysLeuTrpGlyTrpThrMetLeuCysCysAspPheLeuAlaHis 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
146 CTTCAAGTTGTGGGGGTGACAAATGCTGTGTCATTTCCTGGACATTC 195
34 isGlyThrTrpCysTrpThrTrpHisTyrSerGluLysProMetAsnTrp 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
196 ATGGAACGACGCTGACTTACCATTTATTCGAAAAACCATGAACTGG 245

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seq\_name: gb\_est6:AA352567

967  
67 eglnAsnLysAlaGluIleGIuTrfieu.GluUySThrLeuProPhe 82  
+  
|||||  
- |||||  
296 ACANMAACNAGCGGAATTTAGTACTCTGGGAGANAAGACTGCCTTTT 342

seq\_documentation\_block:  
LOCUS AA352567 459 bp mRNA EST 21-Apr-1997  
DEFINITION AS1605078 Activated T-cells XX Homo sapiens cDNA 5' end similar to  
selectin L, mRNA sequence.  
VERSION AA352567.1 GI:2004887  
KEYWORDS  
SOURCE EST.  
ORGANISM human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 459)  
Adams M.D., Kerlavage A.R., Fleischmann R.D., Fulmer R.A., Bull  
C.J., Lee N.H., Kiknes E.F., Weissman R.C., Gocayne J.D., White  
O., Sutton G., Blake J.A., Brandon R.C., Man Wal C., Clayton R.A.,  
Clint F.R., Cotton M.D., Paré-Hughes J., Fine L.D., Fitzgerald  
L.M., Fitzhugh W.M., Fritchman J.L., Geoghegan N.S., Glodok A.,  
Gnehm J.C., Hanna M.C., Hedblom E., Hinkle P.S., Jr., Kelley J.M.,  
Kelley J.C., Liu L.-I., Marcados S.M., Merrick J.M.,  
Moreno-Palances R.F., McDonald L.A., Nguyen D.T., Pelligrino S.M.,  
Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shibley R.,  
Smell K.V., Spriggs T.A., Uterback T.R., Weldman J.F., Li Y.,  
Bednarik D.P., Cao L., Cepeda M.A., Coleman T.A., Collins E.J.,  
Dirke D., Feng D.-F., Ferris A., Fischer C., Hastings G.A., He W.W.,  
Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A.K., Kozak D.L.,  
Kunsch C., Hungjun J., Li H., Meissner P.S., Olsen H., Raymond L.,  
Welf J.F., Wang J., Xu C., Yu G.L., Ruben S.M., Dillon P.J., Fannon  
M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M. and  
Venter J.C.

TITLE Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cDNA sequence  
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
MEDLINE 96026280  
COMMENT Other\_ESTs: THCI72390  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tcdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..459  
/organism="Homo sapiens"  
/db\_xref="ATCC (Inhost):152766"  
/db\_xref="taxon:9606"  
/clone\_id="Activated T-cells XX"  
/cell\_type="T-lymphocyte"  
/dev\_stage="adult"  
/note="Vector: pBluescript SK-, site\_1: EcoRI; site\_2:  
XhoI"

BASE COUNT 137 a 93 c 91 g 132 t 6 others  
ORIGIN

alignment\_scores:  
Quality: 425.00 Length: 81  
Ratio: 5.247 Gaps: 0

Percent Similarity: 100.000      Percent Identity: 100.000

alignment\_block:  
US-09-119-209-2 x AA352567 ..

Align seg 1/1 to: AA352567 from: 1 to: 459

292 G|TThGluLeu|leGlyLysLysLysThr|leGyGluSerSerGly| 308  
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3 GGAACGTAGCTTAATTGGGAAGAAACCAATTTGCAATCATCTGCAAT 52  
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308 e|TSPeAsnProSerPro|leGyGlnLysLeuAspLysSerPheSerG 325  
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53 CTGGTCGAATCTTCTGATCCATATGTCAAAAATTGGACAAAGTTTCTCA 102  
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325 e|lleLysGluGlyAspTyrAsnProLeuPhe|leProValAlaValMet 341  
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103 TGATTAAGGAGGGGTGATTAATACCCCTCTCATTCAGAGGACATGATG 152  
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342 ValThAlaPheSerGlyLeuAlaPhe|le|leTProLeuAlaArgArg 358  
|||||  
153 GTTACGTGCAATCTCTGCTGGCATTAATCATTTGGCTGCAAGAGATTT 202  
|||||  
358 u|LysLysGlyLysLysSerLysArgSerMetLysAsnProTyr 372  
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203 AAAAAAGGCAGAAATCCAGAGAAAGTATGATGATGACCATAT 245  
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seq\_name: gb\_est6:AA355982

seq\_documentation\_block: 279 bp mRNA EST 21-Apr-1997  
LOCUS AA355982  
DEFINITION EST64486 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to  
selectin L, mRNA sequence.  
ACCESSION AA355982  
VERSION AA355982.1 GI:2008322  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 279)  
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fudner,R.A., Bult  
,C.J., Lee,N.H., Kinkness,E.F., Weinschenk,K.G., Gocayne,J.D., White  
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,  
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald  
,L.M., Fitzhugh,W.M., Fritchman,J.L., Georgagen,N.S., Glodok,A.,  
Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,  
Kelley,J.C., Liu,L.-I., Marmaro,S.M., Merrick,J.M.,  
Moreno-Palacios,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,  
Smill,K.V., Spriggs,T.A., Uteback,T.R., Weidman,J.F., Li,Y.,  
Behararik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
DiMiche,D., Feng,D.-F., Ferlie,A., Fischer,C., Hastings,G.A., He,W.W.,  
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,  
Kunsch,C., HungJun,J., Li,H., Weisner,P.S., Olsen,H., Raymond,L.,  
Wel,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon  
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and  
Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cdna sequence  
JOURNAL Nature 377 (6547 Suppl), 3-1/4 (1995)  
MEDLINE 96026280  
COMMENT Other-ESTs: THC172390  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@tigr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/tdb/htgl/htgl.html>)

Seq primer: M13 Reverse.  
Location/Qualifiers  
1..279

FEATURES  
source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/clone\_lib="Jurkat T-cells VI"  
/cell\_type="T-lymphocyte"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 89 a 56 c 69 g 64 t 1 others

ORIGIN

alignment\_scores:  
Quality: 423.00 Length: 73  
Ratio: 5.958 Gaps: 0  
Percent Similarity: 97.260 Percent Identity: 97.260

alignment\_block:  
US-09-119-209-2 x MA355982 ..

Align seg 1/1 to: AA355982 from: 1 to: 279

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17 ephelysteutrpGLYTrpThrMetleucysAspPheleuAlaHisH 34
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102 CTTCAGATTGGGGGTGGACATCTCTGTGTGATTTCCGCGACATC 151
|||||
34 isGLYThrTYrCysTrpThrTYrHisTYrSerGluLysPrometasnTrp 50
|||||
152 ATGGAACCGACTGCTGACTTACCATTTATCGAANAACCATGAACTGG 201
|||||
51 GlnargAlaargArgPheCysArgaspasnTYrThrAspleuValAla1 67
|||||
202 CAAAGGGCTAGAAAGATTCTGCCGAGACATTAACAGANTTATTGTCAT 251
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67 eGlnAsnLysAlaGluLe 73
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252 ACAAAACAAGCGCGAATT 270
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seq_name: gb_est168:BE241595

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seq\_documentation\_block:  
LOCUS BE241595 365 bp mRNA EST 13-JUL-2000  
DEFINITION TCAP1E0689 pediatric acute myelogenous leukemia cell (FAB M1)  
sequence: Baylor-HGSC project-TCOA Homo sapiens cDNA clone TCAP0689, mRNA  
ACCESSION BE241595  
VERSION BE241595.1 GI:9093317  
KEYWORDS EST  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 365)  
Wei, Y., Tsang, Y.T.M., Mei, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.,  
Bouck, J., Gibbs, R.A. and Margolin, J.F.  
Pediatric Leukemia cDNA Sequencing Project  
Unpublished (2000)  
Contact: Dr. Judith F. Margolin  
Human Genome Sequencing Center at Baylor College of Medicine and  
Texas Children's Cancer Center  
One Baylor Plaza, Houston, TX 77030, USA  
Tel: 713 770 4536  
Fax: 713 770 4038  
Email: jmargin@bcm.tmc.org  
Seq primer: M13 primer.  
Location/Qualifiers  
1..365

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="TCAP0689"  
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/sex="male"  
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/lab\_host="DH10B"  
/note="Vector: lambda pSB; Site\_1: BamHI; Site\_2: EcoRI;  
First strand cDNA was primed with an anchored  
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3'; V-A,C,G; N=A,C,G,T] and then dg tailed. Second  
strand was primed with a BamHI-dC primer  
[5'AGAGACTGAGTCGCGCGCGCGCATATATATAT(C) 3']  
Double-stranded cDNA was then digested with BamHI and XhoI  
and directionally cloned into the BamHI and SalI sites of  
lambda pSB vector. Library was constructed by Wei Yu"

BASE COUNT 110 a 81 c 91 g 82 t 1 others

ORIGIN

alignment\_scores:  
Quality: 416.00 Length: 71  
Ratio: 5.943 Gaps: 0  
Percent Similarity: 98.592 Percent Identity: 97.183

alignment\_block:  
US-09-119-209-2 x BE241595 ..

Align seg 1/1 to: BE241595 from: 1 to: 365

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17 ephelysteutrpGLYTrpThrMetleucysAspPheleuAlaHisH 34
|||||
202 CTTCAGATTGGGGGTGGACATCTCTGTGTGATTTCCGCGACATC 251
|||||
34 isGLYThrTYrCysTrpThrTYrHisTYrSerGluLysPrometasnTrp 50
|||||
252 ATGGAACCGACTGCTGACTTACCATTTATCGAANAACCATGAACTGG 301
|||||
51 GlnargAlaargArgPheCysArgaspasnTYrThrAspleuValAla1 67
|||||
302 CAAAGGGCTAGAAAGATTCTGCCGAGACATTAACAGANTTATTGTCAT 351
|||||
67 eGlnAsnLysAla 71
|||||
352 ACAAAACAAGCGCG 364
|||||

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